

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:20:58 ; Search time 23 Seconds

(without alignments)  
20.375 Million cell updates/sec

Title: US-09-914-088-1  
Sequence: 1 EDGQVMDVD 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	428	1 EPC_HUMAN	P01854 homo sapien
2	37	78.7	980	1 NAL7_HUMAN	Q8WX94 homo sapien
3	36	76.6	655	1 SYT_CAUCR	Q9AAX8 caulobacter
4	36	76.6	677	1 BAGS_BOMMO	Q9B136 bombyx mori
5	34	72.3	561	1 DNLI_HAINT	Q9H735 halobacteri
6	34	72.3	841	1 SECA_BACSU	P28366 bacillus su
7	34	72.3	1379	1 TBP7_YEAST	P03340 saccharomyc
8	33	70.2	287	1 DNAL_SYNP7	P50026 synchococcc
9	33	70.2	616	1 ILVD_PHOHL	Q7MYJ5 photorhabdu
10	33	70.2	634	1 NTP1_MCV1	Q98267 molluscum c
11	33	70.2	860	1 GYRA_SYNY3	Q95738 synchocyst
12	33	70.2	877	1 PWT1_CANAL	Q74189 candida alb
13	33	70.2	1119	1 RPOB_THBAQ	Q9KWT7 thermus aqu
14	32	68.1	95	1 CH10_BORPE	P48221 bordetella
15	32	68.1	97	1 RL21_METMA	Q8PNU1 methanosarc
16	32	68.1	121	1 Y408_MERTA	Q57851 methanococc
17	32	68.1	211	1 UPF_PYPAR	Q8ZWW9 pyrobaculum
18	32	68.1	235	1 CAMT_POPEX	Q8ZWW9 pyrobaculum
19	32	68.1	240	1 RR40_YEAST	P07524 streptomyce
20	32	68.1	272	1 TYRO_STRAT	P07524 streptomyce
21	32	68.1	367	1 GCST_MYCTU	Q10376 mycobacteri
22	32	68.1	398	1 AMP1_ARATH	Q9SLM5 arabidopsis
23	32	68.1	485	1 ALGA_PSEPK	Q88ND5 p alginata
24	32	68.1	501	1 VLI_PAPVE	P11326 european el
25	32	68.1	508	1 VLI_HPV1A	P03099 human papil
26	32	68.1	513	1 VLI_PAPVD	P03104 deer papill
27	32	68.1	556	1 ILVD_THBRTN	Q8R3D9 thermomater
28	32	68.1	574	1 ILD2_BRAJA	Q89KX5 bradyrhizob
29	32	68.1	602	1 SYD_TREPA	Q83950 treponema p
30	32	68.1	631	1 NTP1_VACCA	O57214 vaccinia vi
31	32	68.1	631	1 NTP1_VACCC	P20637 vaccinia vi
32	32	68.1	631	1 NTP1_VACCV	P05807 vaccinia vi
33	32	68.1	631	1 NTP1_VARV	P33066 varicella vir

34	32	68.1	631	1 NTP1_YABAM	Q9pb93 yaba monkey
35	32	68.1	699	1 HS82_ORYSA	P33126 oryza sativ
36	32	68.1	1028	1 BGAL_ENTCI	Q47077 enterobacte
37	32	68.1	1828	1 DOCC2_MOUSE	Q8C3J5 mus musculu
38	32	68.1	1830	1 DOCC2_MOUSE	Q92608 homo sapien
39	32	68.1	2035	1 M18A_MOUSE	Q9J1M9 mus musculu
40	32	68.1	2054	1 M18A_HUMAN	Q92614 homo sapien
41	32	68.1	4911	1 M18A_HUMAN	Q92614 homo sapien
42	31.5	67.0	218	1 N1PL_MOUSE	Q922F7 mus musculu
43	31.5	67.0	219	1 N1PL_HUMAN	Q60238 homo sapien
44	31	66.0	109	1 YCIU_SHIFL	Q831d1 shigella fl
45	31	66.0	119	1 RL24_HALMA	P10972 halocarcula

## ALIGNMENTS

RESULT 1	EPC_HUMAN	STANDARD;	PRT;	428 AA.
ID	EPC_HUMAN			
AC	P01854;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	19 epsilon chain C region.			
GN	IGHF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8316897; PubMed=6300763;			
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,			
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;			
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin			
RT	epsilon chain cDNA.";			
RL	Nucleic Acids Res. 11:719-726(1983).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANT LEU-359.			
RX	MEDLINE=83001945; PubMed=6288268;			
RA	Max F.E., Battey J., Ney R., Kirsch I.R., Leder P.;			
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";			
RL	Cell 29:691-699(1982).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84236029; PubMed=6234164;			
RA	Flanagan J.G., Rabbits T.H.;			
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant			
RT	region gene, and evidence for three non-allelic genes.";			
RL	EMBO J. 1:655-660(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84207910; PubMed=6327276;			
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;			
RT	"Long terminal repeat-like elements flank a human immunoglobulin			
RT	epsilon pseudogene that lacks introns.";			
RL	EMBO J. 1:1539-1544(1982).			
RN	[5]			
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).			
RA	Bennich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;			
RL	(in) Bach M.K. (eds.).			
RT	Immediate hypersensitivity: modern concepts and developments, pp.1-36,			
RL	Marcel Dekker, New York (1978).			
RN	[6]			
RP	SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.			
RX	MEDLINE=83065234; PubMed=6815636;			
RA	Kenten U.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,			
RA	Bell L.O., Gould H.J.;			
RT	"Cloning and sequence determination of the gene for the human			
RT	immunoglobulin epsilon chain expressed in a myeloma cell line.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).			
RN	[7]			

RP 3D-STRUCTURE MODELING.  
RX MEDLINE=87089848; PubMed=3796618;  
RA Padlan E.A., Davies D.R.;  
RT "A model of the Fe of immunoglobulin E.",  
RL Mol. Immunol. 23:1063-1075(1986).  
CC -1- SIMILARITY: Contains 4 immunoglobulin-like domains.  
CC -----  
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CC -----  
CC EMBL: I000022; AAB59424.1; ALT\_INIT.  
DR PIR; A22771; EMBL.  
DR PDB; 1IGE; 15-JUL-92.  
DR PDB; 1PP5; 30-JAN-02.  
DR PDB; 1G84; 16-MAY-01.  
DR PDB; 100V; 18-SEP-02.  
DR Genew; HGNC:5522; IGHE.  
DR MIM; 147180; -.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; Ig\_4.  
DR SMART; SM00407; Igcl; 4.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN 6 103  
FT DOMAIN 112 210  
FT DOMAIN 214 318  
FT DOMAIN 324 423  
FT DISULFID 14 14  
FT DISULFID 15 105  
FT DISULFID 29 85  
FT DISULFID 121 121  
FT DISULFID 135 193  
FT DISULFID 209 209  
FT DISULFID 239 299  
FT DISULFID 345 405  
FT CARBOHYD 21 21  
FT CARBOHYD 49 49  
FT CARBOHYD 99 99  
FT CARBOHYD 146 146  
FT CARBOHYD 252 252  
FT CARBOHYD 275 275  
FT VARIANT 359 359  
FT STRAND 110 110  
FT STRAND 113 117  
FT HELIX 122 124  
FT HELIX 125 125  
FT STRAND 130 141  
FT STRAND 146 150  
FT STRAND 155 155  
FT STRAND 159 161  
FT STRAND 165 166  
FT TURN 168 169  
FT STRAND 172 181  
FT STRAND 182 186  
FT TURN 187 188  
FT STRAND 192 196  
FT TURN 198 199  
FT TURN 201 202  
FT STRAND 205 207  
FT STRAND 218 222  
IG-LIKE 1.  
IG-LIKE 2.  
IG-LIKE 3.  
IG-LIKE 4.  
INTERCHAIN (WITH A LIGHT CHAIN).  
INTERCHAIN (WITH A HEAVY CHAIN).  
INTERCHAIN (WITH A HEAVY CHAIN).  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
N-LINKED (GLCNAC. . .).  
W->L (POSSIBLE POLYMORPHISM).  
/FTID=VAR\_00385.

FT TURN 226 229  
FT TURN 231 232  
FT STRAND 236 242  
FT STRAND 252 252  
FT STRAND 255 257  
FT TURN 258 259  
FT STRAND 260 260  
FT TURN 265 266  
FT STRAND 271 274  
FT TURN 275 276  
FT STRAND 277 285  
FT STRAND 288 293  
FT TURN 294 294  
FT STRAND 297 302  
FT TURN 304 305  
FT STRAND 310 314  
FT STRAND 322 322  
FT STRAND 325 329  
FT STRAND 334 337  
FT HELIX 334 337  
FT STRAND 340 348  
FT STRAND 350 351  
FT STRAND 356 360  
FT TURN 366 369  
FT STRAND 374 374  
FT STRAND 377 378  
FT TURN 380 381  
FT STRAND 384 385  
FT STRAND 387 393  
FT STRAND 394 398  
FT TURN 399 400  
FT STRAND 404 408  
FT STRAND 418 421  
SQ SEQUENCE 428 AA; 47019 MW; 25C4CA072AAS58A0 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 428;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQVMDVD 9  
Db 151 EDGQVMDVD 159

RESULT 2  
NAL7 HUMAN STANDARD; PRT; 980 AA.  
ID NAL7 HUMAN  
AC O8W54;  
DT 28-FEB-2003 (Rel. 41, Last Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE NACHT-, LRR- and PYD-containing protein 7 (PYRIN-containing APAF1-like  
DE protein 3).  
GN NALP7 OR PYPAF3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
OX [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22162427; PubMed=12019269;  
RA Wang L., Manji G.A., Grenier J.M., Al-Garawi A., Merriam S.,  
RA Lora J.M., Geddes B.J., Briskin M., Distefano P.S., Bettin J.,  
RA "PYPAF7, a novel PYRIN-containing APAF1-like protein that regulates  
RT activation of NF-kappa B and caspase-1-dependent cytokine  
RT processing".  
RT J. Biol. Chem. 277:29874-29880(2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=2451042; PubMed=12563287;  
RA Tschopp J., Martinon F., Burns K.,  
RT "NALP6: a novel protein family involved in inflammation.";  
RL Nat. Rev. Mol. Cell Biol. 4:95-104(2003).  
CC -1- SIMILARITY: Contains 1 DAPIN domain.

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CC -1- SIMILARITY: Contains 1 NACHT domain.
CC -1- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
CC -----
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CC -----
DR EMBL; AF64765; AAL69963.1; -.
DR EMBL; AY154462; AAO18158.1; -.
DR Genem; HGNC:22947; NALP7.
DR InterPro; IPR007091; LRR_RNinh.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR004020; PAAD_DAPIN_dom.
DR Pfam; PF05729; NACHT; 1.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR PROSITE; PS50824; DAPIN; 1.
DR PROSITE; PS50837; NACHT; 1.
DR ATP-binding; Leucine-rich repeat; Repeat.
KW MAIN 1 93
FT DOMAIN 172 491 DAPIN.
FT REPEAT 614 638 NACHT.
FT REPEAT 674 697 LRR 1.
FT REPEAT 760 784 LRR 2.
FT REPEAT 788 810 LRR 3.
FT REPEAT 817 840 LRR 4.
FT REPEAT 845 868 LRR 5.
FT REPEAT 874 897 LRR 6.
FT REPEAT 902 928 LRR 7.
FT REPEAT 933 957 LRR 8.
FT REPEAT 978 185 LRR 9.
FT NP_BIND 178 185 ATP (POTENTIAL).
SQ SEQUENCE 980 AA; 111806 MW; 822AF2FD4338003D CRC64;

Query Match 78.7%; Score 37; DB 1; Length 980;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 93 EDGQVMDVD 101

RESULT 3
SYT CAUCR STANDARD; PRT; 655 AA.
ID SYT CAUCR
AC Q9AX8;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
DE (Thrs).
GN THRS OR CC0464.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohn A.N., Maddock J.R.,
RA DeBock I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utechtack T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-threonine + tRNA(Thr) = AMP +

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CC diphosphate + L-threonyl-tRNA(Thr).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; AE005719; AAK2451.1; -.
DR PIR; G87306; G87306.
DR HSP; P00955; IEVL.
DR TIGR; CC0464; -.
DR HAMAP; MF_00184; -.
DR InterPro; IPR004154; HGTP_anticonodon.
DR InterPro; IPR004095; TGS_dom.
DR InterPro; IPR002314; tRNA-synt 2b.
DR InterPro; IPR002320; tRNA-synt_thr.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF03129; HGTP_anticonodon; 1.
DR Pfam; PF02824; TGS; 1.
DR Pfam; PF0587; tRNA-synt 2b; 1.
DR PRINTS; PR01047; TRNASYNTHTHR.
DR TIGRFAMs; TIGR00418; thrs; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Zinc; Complete proteome.
FT DOMAIN 248 540 CATALYTIC.
FT METAL 340 340 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 517 517 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 655 AA; 73719 MW; BB75D312CC887799 CRC64;

Query Match 76.6%; Score 36; DB 1; Length 655;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQVMDVD 9
Db 41 DGQVMDVD 48

RESULT 4
BAGS_BOMMO STANDARD; PRT; 677 AA.
ID BAGS_BOMMO
AC Q9BLU6;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE BAG domain-containing protein Samu1.
GN SAMU1.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=N4; TISSUE=EGG;
RX MEDLINE=21315830; PubMed=11422373;
RA Moribe Y., Niml T., Yamashita O., Yaginuma T.;
RA "Samu1, a novel cold-inducible gene, encoding a protein with a BAG
RA domain similar to silence of death domains (SODD/BAG-4), isolated
RT from Bombyx diapause eggs.";
RL Eur. J. Biochem. 268:3432-3442(2001).
CC -1- FUNCTION: May play a role in transmitting a signal which both
CC protects nondiapause eggs from cold injury and terminates diapause
CC in diapause eggs.

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CC -1- SUBUNIT: Binds to HSP70.
CC -1- TISSUE SPECIFICITY: Expressed at high levels in chilled diapause
CC eggs and to a lesser extent in chilled nondiapaused eggs.
CC -1- DEVELOPMENTAL STAGE: In diapause eggs, expressed after chilling at
CC 5 degrees Celsius for 5-6 days, persists for 30 days and then
CC decreases.
CC -1- INDUCTION: By cold.
CC -1- MISCELLANEOUS: 'Samui' means 'cold' in Japanese.
CC -1- SIMILARITY: Contains 1 BAG domain.
CC -----
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CC -----
CC EMBL: AB032717; BAB39763.1; -.
CC GO: GO:0030544; F: HSP70 protein binding; IDA.
CC InterPro: IPR003103; BAG.
CC Pfam: PF02179; BAG; 1.
CC Chapterone; Developmental protein.
CC DOMAIN 22 25 POLY-GLU.
CC FT DOMAIN 103 141 GLN-RICH.
CC FT DOMAIN 233 380 GLN/PRO-RICH.
CC FT DOMAIN 607 643 IYS-RICH.
CC FT DOMAIN 380 457 BAG.
CC SEQUENCE 677 AA; 75979 MW; 3C8374CAFD04FB49 CRC64;

Query Match
Best Local Similarity 76.6%; Score 36; DB 1; Length 677;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DEQVMDVD 9
DB 665 DEQVMDVD 672

RESULT 5
DNTL HALNT
ID DNTL HALNT STANDARD; PRT; 561 AA.
AC 09HR35;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
GN LIG OR VNG0881G.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
(1)
RN SEQUENCE FROM N.A.
RP MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahaitas G.G., Bergquist B., Pan M.,
RA Shukla S., Lasky S.R., Baliga N.S., Thorsson V., Shogana J.,
RA Shukla S., Wei D., Hall U., Dahl T.A., Welti R., Goo Y.A.,
RA Leitauer B., Keller K., Cruz R., Danson M.U., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasarma S.;
RA "Genome sequence of Halobacterium species NRC-1";
RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RL -1- FUNCTION: This protein seals, during DNA replication, DNA
CC recombination and DNA repair, nicks in double-stranded DNA (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: ATP + (deoxyribonucleotide) (N) +
CC (deoxyribonucleotide) (N+M) = AMP + diphosphate +
CC -1- SIMILARITY: Belongs to the ATP-dependent DNA ligase family.
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CC -----
CC EMBL: AF005027; AAG19323.1; -.
CC PIR: G84244; G84244.
CC HAMAP: ME_00407; -.
CC InterPro: IPR000977; DNA_ligase.
CC Pfam: PF01068; DNA_ligase_1.
CC Pfam: PF04679; DNA_ligase_A_C; 1.
CC Pfam: PF04675; DNA_ligase_A_N; 1.
CC TIGRfam: TIGR00574; Gnl1; 1.
CC PROSITE: PS00697; DNA_LIGASE_A1; 1.
CC PROSITE: PS00333; DNA_LIGASE_A2; FALSE_NEG.
CC PROSITE: PS0160; DNA_LIGASE_A3; 1.
CC KW ATP-binding; DNA replication; DNA recombination; Cell division; ligase;
CC ATP-binding; Complete proteome.
CC AMP (BY SIMILARITY).
CC SEQUENCE 561 AA; 59619 MW; 5BB30D3CD106D2E CRC64;

Query Match
Best Local Similarity 72.3%; Score 34; DB 1; Length 561;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9
DB 497 EDQVMDVD 505

RESULT 6
SECA_BACSU
ID SECA_BACSU STANDARD; PRT; 841 AA.
AC P28366;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Preprotein translocase seca subunit.
GN SECA OR DIV+ OR BSU35300.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
(1)
RN SEQUENCE FROM N.A.
RP STRAIN=168 / Marburg;
RC MEDLINE=91192600; PubMed=1901557;
RA Sadate Y., Takamatsu H., Nakamura K., Yamane K.;
RT "Sequencing reveals similarity of the wild-type div+ gene of Bacillus
RT subtilis to the Escherichia coli seca gene.";
RL Gene 98:101-105 (1991).
(2)
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Betteiro M.G., Bessieres P., Bolotin A., Borchet S.,
RA Borris R., Boursier L., Brans A., Braun W., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denicol F., Devine K.M., Dusterhoft A., Enlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita K., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaeser P., Goffeau A., Golligly E.J., Grandi G.,

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RA Guisepi G., Guy B.-J., Haga K., Haelech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Biancard M., Klein C.,  
 RA Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue F.,  
 RA Medina N., Meliado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Paro V., Pohl T.M., Portetelle D., Potwolik S., Prescott A.M.,  
 RA Presecan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Serró S.J., Serró P., Shin B.S., Solido B.,  
 RA Sorokin A., Taccini E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takenchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,  
 RA Tosaio V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,  
 RA Viart A., Wambut R., Wedler H., Weitzenecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zanchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*."  
 RT Nature 390:249-256(1997).

RL Sequence 390:249-256(1997).  
 [4]  
 RP SEQUENCE OF 1-364 FROM N.A.  
 RC STRAIN=ATCC 6057;  
 RX MEDLINE=91375427; PubMed=1832735;  
 RA Overhoff B., Klein M., Spies M., Freund R.;

RT "Identification of a gene fragment which codes for the 364 amino-terminal amino acid residues of a SecA homologue from *Bacillus subtilis*: further evidence for the conservation of the protein export apparatus in Gram-positive and Gram-negative bacteria.";  
 RT Mol. Gen. Genet. 228:417-423(1991).

CC -1- FUNCTION: Involved in protein export. Interacts with the secY/secE subunits. SecA has a central role in coupling the hydrolysis of ATP to the transfer of pre-secretory periplasmic and outer membrane proteins across the membrane.

CC -1- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secD, secE, secF, secG and secY (By similarity).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MEMBRANE, AND CYTOSOL.

CC -1- SIMILARITY: Belongs to the secA family.

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CC EMBL, D10279; BA001122.1; -;  
 CC EMBL, U56901; AAC44957.1; -;  
 CC EMBL, Z99122; CAB15547.1; -;  
 CC EMBL, X62035; CAA43977.1; -;  
 CC PIR, J00647; J00647.  
 CC PDB, 1M6N; 20-SEP-02.  
 CC PDB, 1W74; 20-SEP-02.  
 CC Subtilist; BG10741; secA.  
 CC InterPro; IPR001650; Helicase C.  
 CC InterPro; IPR004027; SEC\_C motif.  
 CC InterPro; IPR000185; SecA.  
 CC Pfam; PR02871; helicase C; 1.  
 CC Pfam; PR02810; SEC-C; 1.  
 CC Pfam; PR01043; SecA protein; 1.  
 CC PRINTS; PR00906; SECA.  
 CC TIGRfam; TIGR00963; secA; 1.  
 CC PROSITE; PS01312; SEC\_A; 1.  
 CC Protein transport; AMP-binding; Membrane; Translocation; Transport;  
 KW Complete proteome; 3d-structure.  
 FT NP\_BIND 100 107 ATP (POTENTIAL).  
 FT CONFID 126 126 V -> I (IN REF. 4).  
 SQ SEQUENCE 841 AA; 95530 MW; 9AAC3630139F5EFF CRO64;

Query Match 72.3%; Score 34; DB 1; Length 841;  
 Best Local Similarity 77.8%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 309 EDGQWVD 317

RESULT 7  
 TBP7 YEAST STANDARD; PRT; 1379 AA.  
 ID TBP7 YEAST  
 AC P40340;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE TBP-binding homolog 7.  
 OS *Yarrowia lipolytica* (Baker's yeast).  
 OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c / FY1679;  
 RA Agostoni Cardone M.L., Lucchini G., Melchiorretto P., Nardese V.,  
 RA Vannoni M., Panzeri L.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c;  
 RA Feldmann H.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP PRELIMINARY SEQUENCE OF 1-1207 FROM N.A.  
 RC STRAIN=S288c;  
 RX MEDLINE=95274317; PubMed=7754704;  
 RA Schmal R., Mannhaupt G., Stucka R., Tauer R., Ehle S.,  
 RA Schwarze C., Vetter I., Feldmann H.;

RT "Identification of a set of yeast genes coding for a novel family of putative ATPases with high similarity to constituents of the 26S protease complex.";  
 RT Yeast 10:1141-1155(1994).  
 CC -1- SIMILARITY: Belongs to the AAA ATPase family.  
 CC -1- SIMILARITY: Contains 1 bromodomain.

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CC EMBL, Y07893; CAA69201.1; -;  
 CC EMBL, Z73055; CAA97300.1; -;  
 CC EMBL, X81072; CAA56963.1; -;  
 CC PIR, S64603; S64603.  
 CC Geronline; 141582; -;  
 CC SGD, S0003502; YTK7.  
 CC InterPro; IPR003593; AAA ATPase.  
 CC InterPro; IPR003959; AAA\_ATPase\_centre.  
 CC InterPro; IPR003960; AAA sub.  
 CC InterPro; IPR001487; Bromodomain.  
 CC Pfam; PF00004; AAA; 1.  
 CC Pfam; PR00439; bromodomain; 1.  
 CC SMART, SM00382; AAA; 1.  
 CC PROSITE; PS00674; AAA; 1.  
 CC PROSITE; PS00633; BROMODOMAIN\_1; FALSE\_NEG.  
 CC PROSITE; PS50014; BROMODOMAIN\_2; 1.  
 KW ATP-binding; Bromodomain.  
 FT DOMAIN 135 139 POLY-GLU.

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FT DOMAIN 157 160 POLY-ARG.
FT 358 361 POLY-ASN.
FT DOMAIN 390 395 POLY-LYS.
FT NP_BIND 454 461 ATP (POTENTIAL) .
FT DOMAIN 737 740 POLY-GLU.
FT 1044 1086 BROMODOMAIN (DIVERGENT) .
FT CONFLICT 70 70 D -> E (IN REF. 2) .
FT CONFLICT 241 241 S -> N (IN REF. 2) .
FT CONFLICT 1016 1016 S -> N (IN REF. 2) .
FT CONFLICT 1142 1142 S -> N (IN REF. 2) .
FT CONFLICT 1153 1153 K -> E (IN REF. 2) .
FT CONFLICT 1276 1276 I -> R (IN REF. 2) .
FT CONFLICT 1283 1283 O -> P (IN REF. 2) .
SQ SEQUENCE 1379 AA; 157406 MW; 31D1F6F87E62E04F CRC64;

Query Match 72.3%; Score 34; DB 1; Length 1379;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQYMDVD 9
Db 57 EDDQYMDKD 65

RESULT 8
DNAJ SYNPF STANDARD; PRT; 287 AA.
ID _DNAJ SYNPF 01-OCT-1996 (Rel. 34, Created)
AC P50026;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chaperone protein dnaJ.
GN DNAJ.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1140;
[1] _
RP SEQUENCE FROM N.A.
RX MEDLINE=97382457; PubMed=9240461;
RA Oguchi K., Nimura K., Yoshikawa H., Takahashi H.;
"Sequence and analysis of a dnaJ homologue gene in cyanobacterium
RT Synecococcus sp. PCC7942."
RL Biochem. Biophys. Res. Commun. 236:461-466(1997).
RN [2]
RP SEQUENCE OF 1-189 FROM N.A.
RX MEDLINE=94271242; PubMed=8003021;
RA Nimura K., Yoshikawa H., Takahashi H.;
"Sequence analysis of the third dnaJ homolog gene in Synecococcus
RT sp. PCC7942."
RL Biochem. Biophys. Res. Commun. 201:848-854(1994).
RN [3]
RP ERRATUM
RX MEDLINE=95110355; PubMed=7811295;
RA Nimura K., Yoshikawa H., Takahashi H.;
Biochem. Biophys. Res. Commun. 205:2016-2017(1994).
RL -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,
the Arpase activity of dnaK (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the dnaJ family.
CC -1- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
EMBL; AB003519; BAA21679.1; -.
DR EMBL; D29968; BAA06235.1; -.
DR PIR; JC5550; JC5550.
DR PIR; PC2306; PC2306.

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DR HSP; P25685; 1HDJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_dep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ_1.
DR Pfam; PF01556; DnaJ_1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR Chaperone; DNA replication; Heat shock.
FT DOMAIN 4 73 J-DOMAIN
SQ SEQUENCE 287 AA; 31980 MW; 2927A269B2E6C546 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 287;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQYMDVD 9
Db 151 EDGRLEVD 159

RESULT 9
ILVD PHOLL STANDARD; PRT; 616 AA.
ID ILVD PHOLL 15-MAR-2004 (Rel. 43, Created)
AC Q7MYJ5;
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
GN ILVD OR PLU4682.
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
[1] _
RP SEQUENCE FROM N.A.
RX STRAIN=RT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taouit S., Bocs S., Boursaux-Bude C., Chaudier M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siglier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
"the genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
CC -1- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
oxobutanoate + H(2)O.
CC -1- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
CC -1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
CC -1- SIMILARITY: Belongs to the ilvd / edd family.
CC -----
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CC -----
EMBL; BX571874; CAE17054.1; -.
DR Photolist; plv4682; -.
DR HAMAP; MF_00012; -.
DR PROSITE; PS00886; ILVD_EDD_1; 1.
DR PROSITE; PS00887; ILVD_EDD_2; 1.
KW Branched-chain amino acid biosynthesis; lyase; Iron; Iron-sulfur;
4Fe-4S; Complete proteome.
FT METAL 122 122 IRON-SULFUR (4FE-4S) (POTENTIAL) .
FT METAL 195 195 IRON-SULFUR (4FE-4S) (POTENTIAL) .
SQ SEQUENCE 616 AA; 65785 MW; 8150D713D04D4172 CRC64;

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Query Match 70.2%; Score 33; DB 1; Length 616;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
 :|:|:|:  
 Db 542 QDGDIDID 550

RESULT 10  
 ID NTP1\_MCV1 STANDARD; PRT; 634 AA.  
 AC 098267;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-MAY-2004 (Rel. 43, Last annotation update)  
 DE Nucleoside triphosphatase I (EC 3.6.1.15) (Nucleoside triphosphate  
 DE phosphohydrolyase I) (NPH I) (MCI100R).  
 GN MCI100L.  
 OS Moluscum contagiosum virus subtype 1 (MCV1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Moluscipoxvirus.  
 OX NCBI\_TaxID=10280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96325459; PubMed=8670425;  
 RA Senkevich T.G., Bugert J.V., Stibler J.R., Koonin E.V., Darai G.,  
 RA Moss B.;  
 RT "genome sequence of a human tumorigenic poxvirus: prediction of  
 RT specific host response-evasion genes";  
 RL Science 273:813-816(1996).  
 CC -1- FUNCTION: SERVES TWO ROLES IN TRANSCRIPTION, IT ACTS IN CONCERT  
 CC WITH VIRAL TERMINATION FACTOR/CAPPING ENZYME TO CATALYZE RELEASE  
 CC OF UUUNUU-CONTAINING NASCENT RNA FROM THE ELONGATION COMPLEX, AND  
 CC IT ACTS BY ITSELF AS A POLYMERASE ELONGATION FACTOR TO FACILITATE  
 CC READTHROUGH OF INTRINSIC PAUSE SITES (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.  
 CC -1- SIMILARITY: Belongs to the helicase family. NPH I subfamily.  
 CC -----  
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 CC -----  
 CC EMBL; U60315; AAC55228.1; -;  
 DR PIR; T30702; T30702.  
 DR InterPro; IPR001410; DEAD.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR InterPro; IPR000330; SNF2\_N.  
 DR Pfam; PF00271; helicase\_C; 1.  
 DR Pfam; PF00176; SNF2\_N; 1.  
 DR SMART; SM00487; DEXDC; 1.  
 DR SMART; SM00490; HELIC; 1.  
 KM Hydrolyase; ATP-binding; Transcription.  
 FT DOMAIN 33 311 SNF2\_N.  
 FT NP BIND 394 480 HELICASE\_C.  
 FT NP BIND 54 61 ATP (BY SIMILARITY).  
 FT SITE 140 143 DEXH BOX.  
 SQ SEQUENCE 634 AA; 72102 MW; B786EFBA17E12F56 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 634;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
 :|:|:|:  
 Db 598 EDGRVTDAD 606

RESULT 11  
 ID GYRA\_SYNY3 STANDARD; PRT; 860 AA.  
 AC 055738;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA gyrase subunit A (EC 5.99.1.3).  
 GN GYRA OR SLR0417.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=11448;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
 RA Sugita M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 RT region from map positions 644 to 924 of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-  
 CC stranded DNA in an ATP-dependent manner and also catalyzes the  
 CC interconversion of other topological isomers of double-stranded  
 CC DNA rings, including catenanes and knotted rings.  
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 CC of double-stranded DNA.  
 CC -1- SUBUNIT: Made up of two chains. The A chain is responsible for DNA  
 CC breakage and rejoining; the B chain catalyzes ATP hydrolysis. The  
 CC enzyme forms an A2B2 tetramer.  
 CC -----  
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 CC -----  
 CC EMBL; D64002; BAA10380.1; -;  
 DR PIR; S76534; S76534.  
 DR HSSP; P09097; IAB4.  
 DR InterPro; IPR005743; DNA\_GYRA.  
 DR InterPro; IPR006691; DNA\_gyraseA\_C.  
 DR InterPro; IPR002205; DNA\_topoisolv.  
 DR Pfam; PF03989; DNA\_gyraseA\_C; 6.  
 DR Pfam; PF00521; DNA\_topoisolv; 1.  
 DR Prodom; PD000742; DNA\_topoisolv; 2.  
 DR SMART; SM00434; TOP4C; 1.  
 DR TIGRfam; TIGR01063; gyra; 1.  
 KM Isomerase; Topoisomerase; DNA-binding; Complete proteome.  
 FT ACT SITE 122 122 DNA CLEAVAGE (BY SIMILARITY).  
 SQ SEQUENCE 860 AA; 95073 MW; 8CE4BE91C4CE874C5 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 860;  
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
 :|:|:|:  
 Db 494 EDGERLDTD 502

RESULT 12  
 ID PMT1\_CANAL STANDARD; PRT; 877 AA.  
 AC 074189;  
 DT 15-UTL-1999 (Rel. 38, Created)  
 DT 15-UTL-1999 (Rel. 38, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Dolichyl-1-phosphate-mannose--protein mannosyltransferase 1  
 DE (EC 2.4.1.109).  
 GN PMT1.

```

OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAF3-1;
RC MEDLINE=98361950; PubMed=9694829;
RA Timpel C., Strahl-Bolsinger S., Ziegelbauer K., Ernst J.F.;
RT "Multiple functions of Pmc1p-mediated protein O-mannosylation in the
RT fungal pathogen Candida albicans.";
RL J. Biol. Chem. 273:20837-20846(1998).
CC -1- FUNCTION: TRANSFERS MANNOSE FROM DOL-P-MANNOSE TO SER OR THR
CC RESIDUES ON PROTEINS.
CC -1- CATALYTIC ACTIVITY: Dolichyl phosphate D-mannose + protein =
CC dolichyl phosphate + O-D-mannosyl-protein.
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 39.
CC -1- SIMILARITY: Contains 3 MIR domains.
-----
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-----
DR EMBL: AF000232; AAC31119.1; -.
DR InterPro: IPR003342; Glyco_trans_39.
DR InterPro: IPR003608; MIR.
DR Pfam: PF02815; MIR; 3.
DR Pfam: PF02366; PMT; 1.
DR SMART; SM00472; MIR; 3.
DR PROSITE; PS50919; MIR; 3.
KW Transferrase; Glycosyltransferase; Glycoprotein; Transmembrane;
KW Endoplasmic reticulum; Repeat; Multigene family.
FT TRANSMEM 109 129 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 226 246 POTENTIAL.
FT TRANSMEM 252 272 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT TRANSMEM 604 624 POTENTIAL.
FT TRANSMEM 643 663 POTENTIAL.
FT TRANSMEM 666 686 POTENTIAL.
FT TRANSMEM 700 720 POTENTIAL.
FT DOMAIN 340 394 MIR 1.
FT DOMAIN 403 462 MIR 2.
FT DOMAIN 472 528 MIR 3.
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 877 AA; 99935 MW; 3B0F6B9C96DC16 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 877;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EDGQVMDVD 9
DB 835 EDQVADVVD 843

RESULT 13
ID PROB_THEAQ STANDARD; PRT; 1119 AA.
AC O9KWU7;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase beta chain (RC 2.7.7.6) (Transcriptase
DE beta chain) (RNA polymerase beta subunit).
GN RPOB.
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RA MEDLINE=99428144; PubMed=10499798;
RA Zhang G., Campbell E.A., Minakhin L., Richter C., Severinov K.,
RA Darst S.A.;
RT "Crystal structure of Thermus aquaticus core RNA polymerase at 3.3 A
RT resolution.";
RL Cell 98:811-824(1999).
CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -1- SUBUNIT: The enzyme consists of the sigma chain and the core
CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
CC beta' chain.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
-----
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-----
DR EMBL: Y19223; CAB65465.2; -.
DR PDB; 1HQW; 07-FEB-01.
DR PDB; 1I9Z; 31-MAY-02.
DR InterPro: IPR007121; RNA_pol_B.
DR InterPro: IPR007644; RNA_pol_Rpb2_1.
DR InterPro: IPR007642; RNA_pol_Rpb2_2.
DR InterPro: IPR007645; RNA_pol_Rpb2_3.
DR InterPro: IPR007120; RNA_pol_Rpb2_6.
DR InterPro: IPR007641; RNA_pol_Rpb2_7.
DR Pfam: PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam: PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam: PF04562; RNA_pol_Rpb2_6; 1.
DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
KW Transferrase; Transcription; DNA-directed RNA polymerase;
KW 3D-structure.
SQ SEQUENCE 1119 AA; 124757 MW; 2CEFE6FA79C77F33 CRC64;

Query Match 70.2%; Score 33; DB 1; Length 1119;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDGQVMDVD 9
DB 599 EDGEVAVKD 607

RESULT 14
ID CH10_BORPE STANDARD; PRT; 95 AA.
AC P48221;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 10 kDa chaparonin (Protein Cpn10) (GroES protein).
GN GROS OR GROS OR CPN10 OR Bp1496 OR BB0963 OR Bp0869.
OS Bordetella pertussis,

```

OS Bordetella bronchiseptica (Alcaligenes bronchisepticus), and  
 OS Bordetella parapertussis.  
 CC Bacteria: Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Alcaligenaceae; Bordetella.  
 CX NCBI\_TaxID=520, 518, 519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.pertussis; STRAIN=Tohama / BP338;  
 RX MEDLINE=95309719; PubMed=7789905;  
 RA Fernandez R.C., Weiss A.A.;  
 RT "Cloning and sequencing of the Bordetella pertussis cpn10/cpn60  
 (groESL) homolog.";  
 RL Gene 158:151-152(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B.pertussis, B.bronchiseptica, and B.parapertussis;  
 RX STRAIN=Tohama 1 / ATCC BAA-589 / NCTC 13251, RB50 / ATCC BAA-588,  
 RC and 12822 / ATCC BAA-587;  
 RX MEDLINE=22827954; PubMed=12910271;  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Baason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsels K.,  
 RA Leather S., Moutle S., Norberczak H., O'Neill S., Ormond D., Price C.,  
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmons M., Skelton V., Squares R., Squares S., Stevens K.,  
 RA Uwin L., Whithead S., Barrett B.G., Maskell D.J.;  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:332-40(2003).  
 CC -!- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses  
 CC the ATPase activity of the latter.  
 CC -!- SUBUNIT: Heptamer of 7 subunits arranged in a ring (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the groES chaperonin family.  
 CC -----  
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 CC -----  
 DR EMBL; U12277; AAA74966.1; -;  
 DR EMBL; BX640421; CAE3757.1; -;  
 DR EMBL; BX640439; CAE31462.1; -;  
 DR EMBL; BX640425; CAE40278.1; -;  
 DR PIR; I40330; I40330.  
 DR HSSP; P05380; I40330.  
 DR HAMAP; MF\_00580; -; 1.  
 DR InterPro; IPR001476; Chaperonin\_Cpn10.  
 DR Pfam; PF00166; Cpn10; 1.  
 DR PRINTS; PR00297; CHAPERONIN10.  
 DR ProDom; PD000566; Chaperonin\_Cpn10; 1.  
 DR PROSITE; PS00681; CHAPERONINS\_CPN10; 1.  
 KW Chaperone; Complete proteome.  
 SQ SEQUENCE 95 AA; 10272 MW; 210A938AF6780D38 CRC64;

Query Match 68.1%; Score 32; DB 1; Length 95;  
 Best Local Similarity 55.6%; Pred. No. 27;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
 |||:::  
 Db 50 EDGKLIPVD 58

RESULT 15  
 RL21\_METWA

ID RL21\_METWA STANDARD; PRT; 97 AA.  
 AC Q8PU2L;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 50S ribosomal protein L21e.  
 GN RPL21E OR M2536.  
 OS Methanosarcina mazei (Methanosarcina frisia).  
 CC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
 CC Methanosarcinaceae; Methanosarcina.  
 CX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Goe1 / Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=22120827; PubMed=12125824;  
 RA Deppenmeier U., Johann A., Hartoch T., Merkl R., Schmitz R.A.,  
 RA Martinez-Arias R., Henne A., Wietzer A., Baumeister S., Jacobi C.,  
 RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,  
 RA Bartscharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,  
 RA Filtz H.-J., Gottschalk G.;  
 RT "The genome of Methanosarcina mazei: evidence for lateral gene  
 RT transfer between Bacteria and Archaea.";  
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).  
 CC -!- SIMILARITY: Belongs to the L21E family of ribosomal proteins.  
 CC -----  
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 CC -----  
 DR EMBL; AE013498; AAM32232.1; -;  
 DR HAMAP; MF\_00369; -; 1.  
 DR InterPro; IPR001147; Ribosomal\_L21e.  
 DR InterPro; IPR008991; Transl\_SH3\_like.  
 DR Pfam; PF01157; Ribosomal\_L21e; 1.  
 DR PROSITE; PS01171; RIBOSOMAL\_L21E; FALSE\_NEG.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 97 AA; 11090 MW; 28FAFEFC0613B5B CRC64;

Query Match 68.1%; Score 32; DB 1; Length 97;  
 Best Local Similarity 55.6%; Pred. No. 28;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
 |||:::  
 Db 35 EDGQWMDVD 43

Search completed: August 23, 2004, 10:37:52  
 Job time : 25 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:30:59 ; Search time 113 Seconds

(without alignments)  
25.130 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQVMDVD 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_ryanus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	80.9	118	17	Q9HPC3
2	38	80.9	249	16	Q828S6
3	37	78.7	341	10	Q7X6W5
4	37	78.7	344	10	Q9ZRD1
5	37	78.7	747	9	Q8SD42
6	37	78.7	1250	5	Q9N595
7	36	76.6	268	16	Q88UT4
8	36	76.6	448	10	Q8LFR0
9	36	76.6	459	16	Q8N021
10	36	76.6	480	10	Q9M2X7
11	36	76.6	487	10	Q8W426
12	36	76.6	487	10	Q7XJ14
13	36	76.6	569	10	Q8LQG1
14	36	76.6	977	5	P91775
15	35	74.5	198	16	Q9P142
16	35	74.5	219	16	Q87Q98

17	35	74.5	265	17	Q26562	Q26562 methanobact
18	35	74.5	358	16	Q9P914	Q9P914 haloarcula
19	35	74.5	470	16	Q7UPD0	Q7UPD0 rhodospirell
20	35	74.5	574	16	Q8F6B9	Q8F6B9 leptospira
21	35	74.5	801	16	Q81RA4	Q81RA4 bacillus an
22	35	74.5	801	16	Q81E55	Q81E55 bacillus ce
23	35	74.5	846	16	Q8YPE6	Q8YPE6 anabaena sp
24	35	74.5	1016	16	Q8CX78	Q8CX78 oceanobacti
25	35	74.5	1222	5	Q81BL4	Q81BL4 plasmodium
26	35	74.5	1275	3	Q9P6A4	Q9P6A4 neurospora
27	35	74.5	2360	5	Q7YZP0	Q7YZP0 elmeria max
28	35	74.5	12268	5	Q8WQ08	Q8WQ08 caenorhabdi
29	35	74.5	13100	5	Q091E5	Q091E5 caenorhabdi
30	34	72.3	94	16	Q8XKC4	Q8XKC4 clostridium
31	34	72.3	178	16	Q8M2J8	Q8M2J8 acanthochei
32	34	72.3	203	16	Q92WL6	Q92WL6 rhizobium m
33	34	72.3	210	10	Q9XRB4	Q9XRB4 arabidopsis
34	34	72.3	250	16	Q81RP7	Q81RP7 bacillus an
35	34	72.3	264	16	Q98R24	Q98R24 mycoplasma
36	34	72.3	267	10	Q7X6S1	Q7X6S1 oryza sativ
37	34	72.3	286	17	Q30057	Q30057 archaeoglob
38	34	72.3	342	16	Q8ENU2	Q8ENU2 oceanobacti
39	34	72.3	388	16	Q87OT2	Q87OT2 vibrio para
40	34	72.3	531	10	Q94HD6	Q94HD6 oryza sativ
41	34	72.3	531	10	Q7XPH1	Q7XPH1 oryza sativ
42	34	72.3	546	2	Q9KVZ8	Q9KVZ8 xanthomonas
43	34	72.3	557	3	Q9Y7B0	Q9Y7B0 yarrowia li
44	34	72.3	571	2	Q8VTS4	Q8VTS4 xanthomonas
45	34	72.3	584	16	Q8R8K6	Q8R8K6 thermotanaer

## ALIGNMENTS

RESULT 1	Q9HPC3	PRELIMINARY	PRT	118 AA.
ID	Q9HPC3	Q9HPC3		
AC	Q9HPC3	Q9HPC3		
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)			
DE	50S ribosomal protein L24P.			
GN	RL24P OR YNG1702G.			
OS	Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).			
OC	Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Halobacterium.			
OX	NCBI_TaxID=64091;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20504483; PubMed=11016950;			
RA	Ng W.V., Kennedy S.P., Mahaitas G.G., Bergquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Meli R., Goo Y.A., Leitman B., Keller K., Cruz R., Danson M., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Bhargava H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., "Genome sequence of Halobacterium species NRC-1"; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).			
RL	EMBL: A8005077; AKG19947.1; -.			
DR	PIR: G84322; G84322.			
DR	PIR: G84322; G84322.			
DR	GO: GO:0005622; C:intracellular; IEA.			
DR	GO: GO:0005840; C:ribosome; IEA.			
DR	GO: GO:0003735; P:structural constituent of ribosome; IEA.			
DR	GO: GO:0006412; P:protein biosynthesis; IEA.			
DR	InterPro: IPR005824; KOW.			
DR	InterPro: IPR006646; KOW sub.			
DR	InterPro: IPR005825; Ribosomal L24_26.			
DR	InterPro: IPR008991; Transl_SH3_like.			
DR	Pfam: PF00467; KOW: 1.			
DR	SMART: SM00739; KOW: 1.			
DR	PROSITE: PS01108; RIBOSOMAL_L24; 1.			

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KM Ribosomal protein; Complete proteome.
SQ SEQUENCE 118 AA; 13369 MW; 90C2F1C4577190A8 CRC64;
Query Match
Best Local Similarity 80.9%; Score 38; DB 17; Length 118;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGQVMDV 9
   |||:|
   59 EDGEVTDV 67

Db

RESULT 2
OQ 082856 PRELIMINARY; PRT; 249 AA.
ID 082856
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative GntR-family transcriptional regulator.
GN SAV6586.
OC Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinoe M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinoe M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RT Nat. Biotechnol. 21:526-531(2003).
RN [3]
RP EMBL; APO05047; BAC74297.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000524; HTH_GntR.
DR Pfam; PF00392; gntR; 1.
DR PRINTS; PR00035; HTHGNT.
DR SMART; SM00345; HTH_GNTR; 1.
KW Complete proteome.
SQ SEQUENCE 249 AA; 27870 MW; 437A662812438B79 CRC64;

Query Match
Best Local Similarity 80.9%; Score 38; DB 16; Length 249;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDV 8
   |||:|
   223 EDGQVLDV 230

Db

RESULT 3
OQ 07X6W5 PRELIMINARY; PRT; 341 AA.
ID 07X6W5
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE OSJNB0086G13.4 protein (OSJNB0088K19.15 protein).
SQ SEQUENCE 341 AA; 35526 MW; 1B82761A54266AF3 CRC64;

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GN OSJNB0086G13.4 OR OSJNB0088K19.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia Y., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang D.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Pan D.L., Meng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RT Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL; AL606706; CAD41026.1; -
DR EMBL; AL606626; CAB03213.1; -
SQ SEQUENCE 341 AA; 35526 MW; AFD3CECFCE1AABC CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 10; Length 341;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDGQVMDV 9
   |||:|
   135 EDGEVTDV 143

Db

RESULT 4
OQ 09ZRD1 PRELIMINARY; PRT; 344 AA.
ID 09ZRD1
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE NTGp4 (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Biemann B.U., Price J.R., Crowell D.N., Randall S.K.;
RT "A collection of cDNAs encoding isoprenylated plant proteins."
RT Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RL EMBL; U64925; AAD09518.1; -
DR HSSP; P02649; ILE4.
DR InterPro; IPR006703; AIG1.
DR Pfam; PF04548; AIG1; 1.
FT NON_TER
SQ SEQUENCE 344 AA; 38526 MW; 1B82761A54266AF3 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 10; Length 344;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDV 8
   |||:|
   69 EDGQVLDV 76

Db

RESULT 5
OQ 08SD42 PRELIMINARY; PRT; 747 AA.
ID 08SD42
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE PHIK2120.
SQ SEQUENCE 747 AA; 80526 MW; 1B82761A54266AF3 CRC64;

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OS Pseudomonas phage phiKZ.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=169683;
RN
RP
RP SEQUENCE FROM N.A.
RA MEDLINE=21914557; PubMed=11916376;
RA Mesanzhinov V.V., Robben J., Grymoprez B., Kostyuchenko V.A.,
RA Bourkaltseva M.V., Sykylinda N.N., Krylov V.V., Volkasert G.,
RT "The genome of bacteriophage phiK2 of Pseudomonas aeruginosa.";
RL J. Mol. Biol. 317:1-19(2002).
RN
RP
RP SEQUENCE FROM N.A.
RA Mesanzhinov V.V., Robben J., Grymoprez B., Kostyuchenko V.A.,
RA Bourkaltseva M.V., Sykylinda N.N., Krylov V.V., Volkasert G.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399011; AAL83021.1; -.
SQ SEQUENCE 747 AA; 82929 MW; 60726E8A39B5C853 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 9; Length 747;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 EDGQYMD 7
|||
Db 429 EDGQYMD 435

RESULT 6
Q9N595 PRELIMINARY; PRT; 1250 AA.
ID Q9N595
AC Q9N595;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Y110A7A.16.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
None;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN
RP
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Ozerksy P., Wohlmann P., Carter T.;
RT "The sequence of C. elegans cosmid Y110A7A.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN
RP
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Waterston R.;
RT "Direct Submission.";
RL Submitted (SRP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006708; AAF60430.2; -.
DR WormPep; Y110A7A.16; CE28103.
DR InterPro; IPR006849; IKI3.
DR Pfam; PF04762; IKI3; 1.
KM Hypothetical protein.
SQ SEQUENCE 1250 AA; 142709 MW; AAF1EDA831727DED CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 5; Length 1250;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQYMD 9
|||:||||:

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Db          88 EDGEVMDLE 96

RESULT 7
Q88UY4      PRELIMINARY;      PRT;      268 AA.
AC Q88UY4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Septum site-determining protein Mnd.
MIND OR LP 2315.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxId=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 9826 / WCFS1;
RX MEDLINE=22480296; PubMed=1256566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers M.E.U., Stiekema W., Klein Hankorst R.M., Bron P.A.,
RA Hotter S.M., Niepof Groot M.N., Kerkhoven R., De Vries M., Usting B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003) .
DR EMBL; AL935258; CAD64640.1; -
DR InterPro: IPR000707; ATPase_Para.
KW Pfam; PF00991; Para; 1.
SQ SEQUENCE 268 AA; 29100 MM; D3CE7F19A27609FC CRC64;

Query Match          76.6%; Score 36; DB 16; Length 268;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
   :|:|:|:|
Db 182 QDGETMDID 190

RESULT 8
Q8LFRO      PRELIMINARY;      PRT;      448 AA.
AC Q8LFRO;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Hypothetical protein.
OS Arabidopsis thaliana (Mouse-ear cress) .
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucots II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
annotation ";
RL Genome Biol. 0:0-0(2002) .
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana ";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY084697; AAM61258.1; -.
DR InterPro: IPR008936; ARM.
DR InterPro: IPR003613; ZnF_modRING.
KW Pfam; PF04564; U-Dox; 1.
SMART; SM00504; Ubox; 1.

```

KW Hypothetical protein.  
 SQ SEQUENCE 448 AA; 49011 MW; 4AD6978DE54F763 CRC64;  
 Query Match 76.6%; Score 36; DB 10; Length 448;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGVMDVD 9  
 |||:|:  
 Db 20 DQGVMDLD 27

RESULT 9  
 Q8N021 PRELIMINARY; PRT; 459 AA.  
 ID Q8N021; PRELIMINARY; PRT; 459 AA.  
 AC Q8N021; PRELIMINARY; PRT; 459 AA.  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Uncharacterized ATPase related to the helicase subunit of the holliday junction resolvase.  
 DE CGLI633.  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
 CX NCBI\_TaxId=1718;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
 RA Nakagawa S.;  
 RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DT EMBL; AP005279; BAB99026.1; -  
 DR GO; GO:0005653; C:DNA replication factor C complex; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0004386; F:helicase activity; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR InterPro; IPR003959; AAA\_ATPase-centr.  
 DR InterPro; IPR000862; Pfcdomain.  
 DR Pfam; PF00004; AAA; 1.  
 KW Helicase; Complete proteome.  
 SQ SEQUENCE 459 AA; 49478 MW; 8965BDF6A27594DE CRC64;

Query Match 76.6%; Score 36; DB 16; Length 459;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQGVMDVD 9  
 |||:|:  
 Db 245 EDQGVMDLD 253

RESULT 10  
 Q9M2X7 PRELIMINARY; PRT; 480 AA.  
 ID Q9M2X7; PRELIMINARY; PRT; 480 AA.  
 AC Q9M2X7; PRELIMINARY; PRT; 480 AA.  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 DE T16K5.160.  
 GN T16K5.160.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 CX NCBI\_TaxId=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,  
 RA Newes H.W., Lemcke K., Mayer K.F.X., Queiter F., Salanoubat M.;  
 RA Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL132965; CAB66919.1; -  
 DR PIR; T46047; T46047.  
 DR InterPro; IPR008938; ARM.  
 DR InterPro; IPR003613; Znf\_modRING.  
 DR Pfam; PF04564; U-box; 1.  
 DR SMART; SM00504; Ubox; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 480 AA; 52645 MW; CC54E011E9306F8A CRC64;

Query Match 76.6%; Score 36; DB 10; Length 480;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGVMDVD 9  
 |||:|:  
 Db 20 DQGVMDLD 27

RESULT 11  
 Q8W426 PRELIMINARY; PRT; 487 AA.  
 ID Q8W426; PRELIMINARY; PRT; 487 AA.  
 AC Q8W426; PRELIMINARY; PRT; 487 AA.  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE 21D7.  
 GN OS21D7.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 CX NCBI\_TaxId=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Yanagawa Y., Hasegawa S., Kumagai F., Fujimuro M., Yokosawa H.,  
 RA Tanaka K., Komamine A., Hashimoto J., Sato T., Nakagawa H.;  
 RT "Colocalization of proteasome subunits and plant specific microtubules, preprophase bands and phragmoplast, during cell cycle."  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB031299; BAB82474.1; -  
 DR Gramene; Q8W426; -  
 DR InterPro; IPR000717; PCI.  
 DR InterPro; IPR008941; TPR-like.  
 DR Pfam; PF01399; PCI; 1.  
 DR SMART; SM00088; PINT; 1.  
 SQ SEQUENCE 487 AA; 54980 MW; 98911593A4832AC1 CRC64;

Query Match 76.6%; Score 36; DB 10; Length 487;  
 Best Local Similarity 77.8%; Pred. No. 1.6e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDQGVMDVD 9  
 |||:|:  
 Db 91 EDQSEMDVD 99

RESULT 12  
 Q7XJ14 PRELIMINARY; PRT; 487 AA.  
 ID Q7XJ14; PRELIMINARY; PRT; 487 AA.  
 AC Q7XJ14; PRELIMINARY; PRT; 487 AA.  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Putative 26S proteasome non-ATPase regulatory subunit 3.  
 DE P0478E02.12.  
 GN P0478E02.12.  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.

```
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Oliveira A.C., Mattoos L.T., Carvalho F.F., Shimano A., Zimmer F.D.,
RT "Oryza sativa nipponbare genomic DNA, chromosome 9, PAC
RT clone: p0478E02."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB109206; BAC79193.1; -.
KW Proteosome.
SQ SEQUENCE 487 AA; 54980 MW; 98911593A4832AC1 CRC64;

Query Match 76.6%; Score 36; DB 10; Length 487;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 91 EDGSEMDVD 99

RESULT 13
Q8LOG1 PRELIMINARY; PRT; 569 AA.
ID 08LOG1
AC 08LOG1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Vacuolar sorting receptor-like protein.
GN P0004D12.8.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0004D12."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003433; BAB92664.1; -.
DR Gramene; O8LOG1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003137; PA.
DR InterPro; IPR006639; Peptidase_A22.
DR InterPro; IPR007369; Peptidase_A22B.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04258; Peptidase_A22B; 1.
DR SMART; SM00730; PSN; 1.
DR KMW.
SQ SEQUENCE 569 AA; 61340 MW; 96967EFA8A8951B CRC64;

Query Match 76.6%; Score 36; DB 10; Length 569;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 148 EDGQVLRVD 156

RESULT 14
P91775 PRELIMINARY; PRT; 977 AA.
AC P91775;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
```

```
DE Pacifastin heavy chain precursor.
OS Pacifastacus leniusculus (Signal crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Astacidae; Pacifastacus.
OX NCBI_TaxID=6720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97338078; PubMed=9192625;
RA Liang Z., Sottrup-Jensen L., Asparn A., Hall M., Soderhall K.;
RT "Pacifastin, a novel 155-kDa heterodimeric proteinase inhibitor
RT containing a unique transferrin chain."
RL Proc. Natl. Acad. Sci. U.S.A. 94:6682-6687(1997).
DR EMBL; U81824; AAC64660.1; -.
DR HSSP; P56410; IAOV.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; F:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR01156; Transferrin.
DR Pfam; PF00405; transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
KM Signal.
FT SIGNAL.
FT CHAIN 23 977 POTENTIAL.
SQ SEQUENCE 977 AA; 106866 MW; 5E81706133350E99 CRC64;

Query Match 76.6%; Score 36; DB 5; Length 977;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 935 EDGHYDID 943

RESULT 15
Q9PI42 PRELIMINARY; PRT; 198 AA.
ID 09PI42
AC 09PI42;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative transcriptional regulator.
GN C70466.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
RA Jags J., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrall B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL; AL139075; CAB75104.1; -.
DR PIR; E81391; E81391.
DR InterPro; IPR000595; CNMP binding.
DR Pfam; PF00027; CNMP_binding; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW Complete proteome.
SQ SEQUENCE 198 AA; 23221 MW; 765B32B63810A030 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 198;
```

Best Local Similarity 44.4%; Pred. No. 97;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDGQYMDVD 9  
|||:::|  
Db 83 EDGEILEID 91

Search completed: August 23, 2004, 10:39:55  
Job time : 118 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: August 23, 2004, 10:20:08 ; Search time 124 Seconds

(without alignments)  
20.507 Million cell updates/sec

Title: US-09-914-088-1  
Sequence: 1 EDGQVMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: geneseq\_29Jan04:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	3 AAB25907	Aab25907 IGE C-eps
2	47	100.0	9	3 AAB20867	Aab20867 Immunoglob
3	47	100.0	9	4 AAB51023	Aab51023 IGE pepti
4	47	100.0	9	4 AAB51023	Aab51023 IGE pepti
5	47	100.0	9	5 AAB00217	Aab00217 Human IGE
6	47	100.0	9	7 AAB00217	Aab00217 Human IGE
7	47	100.0	10	3 AAB25929	Aab25929 PI mimoto
8	47	100.0	10	4 AAB16654	Aab16654 Peptide P
9	47	100.0	10	5 AAB100228	Aab100228 Human IGE
10	47	100.0	10	7 AAB100228	Aab100228 Human IGE
11	47	100.0	13	3 AAB25916	Aab25916 PI mimoto
12	47	100.0	13	3 AAB25916	Aab25916 PI mimoto
13	47	100.0	13	3 AAB25917	Aab25917 PI mimoto
14	47	100.0	13	3 AAB20872	Aab20872 Antialler
15	47	100.0	13	4 AAB51028	Aab51028 IGE pepti
16	47	100.0	13	4 AAB16642	Aab16642 Peptide P
17	47	100.0	13	4 AAB16639	Aab16639 Peptide P
18	47	100.0	13	4 AAB16641	Aab16641 Peptide P
19	47	100.0	13	5 AAB100312	Aab100312 Human IGE
20	47	100.0	13	5 AAB100224	Aab100224 Human IGE
21	47	100.0	13	5 AAB100226	Aab100226 Human IGE
22	47	100.0	14	5 AAB100540	Aab100540 Human IGE
23	47	100.0	16	5 AAB100542	Aab100542 Human IGE
24	47	100.0	20	5 AAB25921	Aab25921 PI mimoto
25	47	100.0	20	3 AAB25971	Aab25971 PI mimoto

26	47	100.0	20	3 AAB23440	Aab23440 Human IGE
27	47	100.0	20	4 AAB16646	Aab16646 Peptide P
28	47	100.0	20	4 AAB16696	Aab16696 Peptide P
29	47	100.0	20	5 AAB100544	Aab100544 Human IGE
30	47	100.0	20	5 AAB100316	Aab100316 Human IGE
31	47	100.0	20	5 AAB100358	Aab100358 Human IGE
32	47	100.0	21	3 AAB25972	Aab25972 PI mimoto
33	47	100.0	21	3 AAB25922	Aab25922 PI mimoto
34	47	100.0	21	4 AAB16647	Aab16647 Peptide P
35	47	100.0	21	4 AAB16647	Aab16647 Peptide P
36	47	100.0	21	5 AAB100359	Aab100359 Human IGE
37	47	100.0	21	5 AAB100317	Aab100317 Human IGE
38	47	100.0	22	3 AAB25920	Aab25920 PI mimoto
39	47	100.0	22	4 AAB16645	Aab16645 Peptide P
40	47	100.0	22	5 AAB100543	Aab100543 Human IGE
41	47	100.0	22	5 AAB100315	Aab100315 Human IGE
42	47	100.0	98	2 AAB85588	Aab85588 Fc(epsilo
43	47	100.0	106	2 AAB85587	Aab85587 Fc(epsilo
44	47	100.0	128	6 AAB74778	Aab74778 Human mod
45	47	100.0	236	6 AAB74780	Aab74780 Human mod

## ALIGNMENTS

RESULT 1  
AAB25907 standard; peptide; 9 AA.  
ID AAB25907  
XX  
AC AAB25907;  
XX  
DT 05-JAN-2001 (first entry)  
XX  
DE IGE C-epsilon-2 domain surface exposed epitope peptide P1 SEQ ID NO:1.  
XX  
KW Epitope: mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;  
KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.  
XX  
XX Homo sapiens.  
XX  
XX WO200050460-A1.  
XX  
XX 31-AUG-2000.  
XX  
XX 22-FEB-2000; 2000MO-EP001455.  
XX  
XX 25-FEB-1999; 99GB-00004405.  
XX  
XX 29-MAR-1999; 99GB-00007151.  
XX  
XX 07-MAY-1999; 99GB-00010537.  
XX  
XX 07-MAY-1999; 99GB-00010538.  
XX  
XX 07-AUG-1999; 99GB-00018594.  
XX  
XX 07-AUG-1999; 99GB-00018603.  
XX  
XX 07-SRP-1999; 99GB-00021046.  
XX  
XX 07-SRP-1999; 99GB-00021047.  
XX  
XX 29-OCT-1999; 99GB-00025619.  
XX  
XX 23-NOV-1999; 99GB-00027698.  
XX  
XX (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
XX Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Bassolac;  
XX WPI; 2000-572073/53.  
XX  
XX Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E.  
XX  
XX Claim 2; Page 5; 129pp; English.

CC The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can  
CC have anti-allergic and immunosuppressive activities, and can be used as a  
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
CC in medicine and in the manufacture of medicaments for treating and  
CC preventing allergies. (IV) is useful for identifying mimotopes of PI, in  
CC medicine and also in manufacturing medicaments for treating allergies.  
CC (II) is useful in diagnostics and in the affinity purification of  
CC circulating anti-IgE antibodies from blood. (II), (III) and PC are useful  
CC for treating a patient susceptible to or suffering from allergies. (IV)  
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention  
CC

SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
|||||  
1 EDGQVMDVD 9RESULT 2  
AAB20867  
ID AAB20867 standard; peptide; 9 AA.

AC AAB20867;

DT 03-JAN-2001 (first entry)

DE Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.

XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;  
XX prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
KW malaria; cytostatic; anti-allergic; nootropic; neuroprotective;  
KW protozoicide; Alzheimer's disease; allergy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200050077-A1.  
PN  
XX  
XX 31-AUG-2000.  
PD

PF 22-FEB-2000; 2000MO-EP001457.

PR 25-FEB-1999; 99GB-00004405.

PR 25-FEB-1999; 99GB-00004408.

PR 25-FEB-1999; 99GB-00004412.

PR 13-AUG-1999; 99GB-00019260.

PA (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Coste M, Lobet Y, Van-Mechelen MP, Veriest C;

WPI; 2000-572040/53.

XX Immunogens and vaccine comprising the immunogen useful for preventing and  
PT treating infectious diseases e.g. malaria and chronic disease e.g.  
PT cancer, comprises peptide and carrier from protein D of influenzae.  
XX

PS Claim 9; Page 37; 53pp; English.

XX The present invention describes an immunogen (I) comprising a peptide  
CC (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae

CC or its fragment. Also described are: (1) a vaccine comprising (I), and an  
CC excipient; (2) preparation of (I) comprising conjugating a peptide to  
CC protein D or its fragment; and (3) preparation of a vaccine of (1),  
CC comprising formulating (I) with an excipient. (I) has cytostatic,  
CC anti-allergic, nootropic, neuroprotective and protozoicide activities. (I)  
CC and the vaccine are useful for the manufacture of a medicament for  
CC preventing and treating infectious diseases such as malaria or chronic  
CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
CC Unlike prior art immunogens, (I) induces high levels of antipeptide  
CC immune responses while inducing a moderate humoral response against the  
CC carrier. The present sequence represents a specifically claimed  
CC immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can be  
CC used in an immunogen of the present invention  
CC

SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
|||||  
1 EDGQVMDVD 9RESULT 3  
AAB51023  
ID AAB51023 standard; peptide; 9 AA.

AC AAB51023;

DT 21-MAR-2001 (first entry)

DE IgE peptide #1.

KW Vaccine; immunoglobulin E; IgE; anti-allergy.

OS Mammalia.

PN WO200074716-A2.

XX 14-DEC-2000.

PF 06-JUN-2000; 2000MO-EP005164.

PR 08-JUN-1999; 99GB-00013327.

PA (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Prieels J;

WPI; 2001-091150/10.

XX New vaccine comprising allergy peptides linked by an inert carrier,  
PT useful for boosting an anti-allergy immune response in an individual  
PT susceptible to an allergic response.  
XX

PS Claim 5; Page 20; 26pp; English.

XX The present invention relates to a composition comprising allergy  
CC peptides linked by an inert carrier. The allergy peptides are derived  
CC from immunoglobulin E (IgE) or IgE receptor. The present peptide is one  
CC such peptide from IgE. The composition is useful as a vaccine or for  
CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
CC In particular, for boosting an anti-allergy immune response in an  
CC individual susceptible to an allergic response  
CC

SQ Sequence 9 AA;

Query Match 100.0%; Score 47; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
DB 1 EDGQVMDVD 9

## RESULT 4

AAU16632 standard; peptide; 9 AA.

AAU16632;

07-NOV-2001 (first entry)

Peptide P1 derived from Cepsilon2 region of human IGF.

Human; linkage technology; conjugated compound; carrier vehicle; epitope;  
Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGF mediated disease;  
antibody response.

Homo sapiens.

WO200145745-A2.

28-JUN-2001.

21-DEC-2000; 2000WO-GH004935.

21-DEC-1999; 99GB-00030233.

22-FEB-2000; 2000GB-00004096.

22-AUG-2000; 2000GB-00020707.

22-AUG-2000; 2000GB-00020708.

(ACAM-) ACAMBI5 RES LTD.  
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Flinn N, Johnson T;

WPI; 2001-521967/57.  
A linkage comprising an immunogenic conjugate useful treatment of IGF  
mediated diseases.

Example 4; Page 21; 48pp; English.

The present invention relates to linkage methodology for use in the  
conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.  
macromolecules, polymers, dendrimers, proteins) to produce biological and  
immunological constructs. The invention provides a method for linking an  
epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a  
pharmaceutical composition or a vaccine. The invention describes peptides  
derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4  
regions of human immunoglobulin E (IgE) which are used to produce  
conjugated compounds. The compounds or compositions of the invention are  
useful in the manufacture of a medicament for the treatment of IGF  
mediated diseases. The invention allows for controlled conjugation of a  
peptide epitope (antigen) to a protein so as to form an immunogenic  
conjugate which may be able to raise a protective antibody response in an  
animal or human patient. AAU16632-AAU16913 represent peptides derived  
from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human  
IgE

Sequence 9 AA;

Query Match 100.0%; Score 47; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
DB 1 EDGQVMDVD 9

RESULT 5

ABJ00217  
ID ABJ00217 standard; peptide; 9 AA.

ABJ00217;

02-SEP-2002 (first entry)

Human IGF immunogenic peptide SEQ ID NO: 1.

Immunogen; human; IGF; immunoglobulin E; allergy; thio-ether linkage;  
vaccine; anti-allergic.

Homo sapiens.

WO200216409-A2.

28-FEB-2002.

17-AUG-2001; 2001WO-EP009576.

22-AUG-2000; 2000GB-00020717.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
(PEPT-) PEPTIDE THERAPEUTICS LTD.

Friede M, Mason S, Turnell WG, Vinals Y Baassisc;

WPI; 2002-489648/52.

Conjugate for use in vaccine for treatment of allergy, comprises  
disulfide bridge cyclized peptide and immunogenic carrier.

Claim 4; Page 9; 45pp; English.

The present invention relates to conjugates suitable for use in vaccines,  
where the conjugate comprises a disulfide bridge cyclized peptide and an  
immunogenic carrier. The vaccines can be used in the treatment of  
allergies. The present sequence is a peptide immunogen derived from human  
immunoglobulin E (IgE) suitable to be cyclised and used in the invention

Sequence 9 AA;

Query Match 100.0%; Score 47; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
DB 1 EDGQVMDVD 9

## RESULT 6

ADE10893  
ID ADE10893 standard; peptide; 9 AA.

ADE10893;

29-JAN-2004 (first entry)

Chimeric hepatitis B virus related B-cell epitope seqid 127.

hepatotropic; virucide; anti-inflammatory; chronic hepatitis; vaccine;  
recombinant hepatitis B core chimeric protein; HBc chimeric protein;  
hepatitis B infection; T-cell stimulator; B-cell epitope.

Homo sapiens.

US2003198645-A1.

23-OCT-2003.

21-FEB-2003; 2003US-00372076.

PR 21-FEB-2002; 2002US-00080299.  
 PR 21-FEB-2002; 2002US-00082014.  
 XX (PAGE/) PAGE M.  
 PA (FRIE/) FRIEDE M.  
 XX Page M, Friede M;  
 XI WPI; 2003-852775/79.  
 DR WPI; 2003-852775/79.  
 XX  
 XX Treating chronic hepatitis B infection by administering a T cell-  
 PT stimulating vaccine containing immunogenic particles having recombinant  
 PT carboxy-terminal truncated hepatitis B core (HBC) chimeric protein  
 PT molecules.  
 XX  
 XX Disclosure; SEQ ID NO 127; 111pp; English.  
 PS  
 PS The invention describes a method of treating chronic hepatitis comprising  
 CC administering to a patient a T cell-stimulating amount of a vaccine  
 CC comprising immunogenic particles dissolved or dispersed in a diluent,  
 CC where the immunogenic particles consists of recombinant hepatitis B core  
 CC (HBC) chimeric protein molecules, and maintaining the patient to induce T  
 CC cells activated against HBC. The methods and compositions of the present  
 CC invention are useful for treating chronic hepatitis B infection. This is  
 CC the amino acid sequence of a chimeric hepatitis B virus related B-cell  
 CC epitope useful for expression within the HBV chimera at the N-terminus,  
 CC within the immunogenic loop and/or at the C-terminus.  
 CC  
 CC Sequence 9 AA;  
 SQ

Query Match Score 47; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EDGQVMDVD 9  
 |||||  
 1 EDGQVMDVD 9  
 Db

RESULT 7  
 AAB25929  
 ID AAB25929 standard; peptide; 10 AA.  
 XX  
 AC AAB25929;  
 XX  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE P1 mimotope peptide P1st SEQ ID NO:23.  
 XX

KW Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;  
 KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
 KW allergy; atopy.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200050460-A1.  
 XX

PD 31-AUG-2000.  
 XX

PF 22-FEB-2000; 2000WO-EP001455.  
 XX

PR 25-FEB-1999; 99GB-00004405.  
 XX

PR 29-MAR-1999; 99GB-00007151.  
 XX

PR 07-MAY-1999; 99GB-00010537.  
 XX

PR 07-AUG-1999; 99GB-00018594.  
 XX

PR 07-SEP-1999; 99GB-00021046.  
 XX

PR 07-SEP-1999; 99GB-00021047.  
 XX

PR 29-OCT-1999; 99GB-00025619.  
 XX

PR 23-NOV-1999; 99GB-00027698.  
 XX

PA (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 XX Dyson M, Friede M, Greenwood J, Hewitt B, Lamont A, Mason S;  
 XI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Bassolsc;  
 XX WPI; 2000-572073/53.  
 XX

PT Peptides useful for treating, preventing and ameliorating allergic  
 PT diseases, comprising an isolated surface exposed group of a specific  
 PT domain from immunoglobulin E.  
 XX

PS Disclosure; Page 9; 129pp; English.  
 XX

CC The present invention describes a peptide (I) comprising an isolated  
 CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of  
 CC immunoglobulin E (IGE), or its mimotope. Also described are: (1) an  
 CC immunogen (II) for treating allergy comprising (II); (2) a vaccine (III)  
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
 CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);  
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (1) can  
 CC have antiallergic and immunosuppressive activities and can be used as a  
 CC vaccine and histamine release inhibitor. (II), (III) and (IV) are useful  
 CC in medicine and in the manufacture of medicaments for treating and  
 CC preventing allergies. (IV) is useful for identifying mimotopes of PI, in  
 CC medicine and also in manufacturing medicaments for treating allergies.  
 CC (II) is useful in diagnostics and in the affinity purification of  
 CC circulating anti-IGE antibodies from blood. (II) (III) and PC are useful  
 CC for treating a patient susceptible to or suffering from allergies. (IV)  
 CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
 CC peptide sequences which are used in the exemplification of the present  
 CC invention  
 CC  
 CC Sequence 10 AA;  
 SQ

Query Match Score 47; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EDGQVMDVD 9  
 |||||  
 2 EDGQVMDVD 10  
 Db

RESULT 8  
 AAU16654  
 ID AAU16654 standard; peptide; 10 AA.  
 XX  
 AC AAU16654;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX

DE Peptide P1st derived as mimotope of Cepsilon2 region of human IGE.  
 XX

KW Human; linkage technology; conjugated compound; carrier vehicle; epitope;  
 KW Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGE mediated disease;  
 KW antibody response.  
 XX

OS Homo sapiens.  
 XX  
 OS Synthetic.  
 XX

PN WO200145745-A2.  
 XX

PD 28-JUN-2001.  
 XX

PF 21-DEC-2000; 2000WO-GB004935.  
 XX

PR 21-DEC-1999; 99GB-00030233.  
 XX

PR 22-FEB-2000; 2000GB-00004096.  
 XX

PR 22-AUG-2000; 2000GB-00020707.  
 XX

PR 22-AUG-2000; 2000GB-00020708.  
 XX



PA (ACAM-) ACAMBI5 RES LTD.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PI Flinn N, Johnson T;  
XX WPI; 2001-521967/57.  
XX A linkage comprising an immunogenic conjugate useful treatment of Ige  
PT mediated diseases.  
XX  
XX  
PS Example 4; Page 21; 48pp; English.  
XX  
CC The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.  
CC macromolecules, polymers, dendrimers, proteins) to produce biological and  
CC immunological constructs. The invention provides a method for linking an  
CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a  
CC pharmaceutical composition or a vaccine. The invention describes peptides  
CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4  
CC regions of human immunoglobulin E (Ige) which are used to produce  
CC conjugated compounds. The compounds or compositions of the invention are  
CC useful in the manufacture of a medicament for the treatment of Ige  
CC mediated diseases. The invention allows for controlled conjugation of a  
CC peptide epitope (antigen) to a protein so as to form an immunogenic  
CC conjugate which may be able to raise a protective antibody response in an  
CC animal or human patient. AAU6632-AAU6513 represent peptides derived  
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human  
CC IGB  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 47; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQVMDVD 9  
|||  
2 EDGQVMDVD 10  
Db

RESULT 9  
ABJ00228  
ID ABJ00228 standard; peptide; 10 AA.  
XX  
AC ABJ00228;  
XX  
DT 02-SBP-2002 (first entry)  
XX  
XX Human Ige immunogenic peptide SEQ ID NO: 12.  
XX  
DE Immunogen; human; Ige; immunoglobulin E; allergy; thio-ether linkage;  
XX  
KW vaccine; antiallergic.  
XX  
XX Homo sapiens.  
XX  
XX MO200216409-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-EP009576.  
XX  
XX 22-AUG-2000; 2000GB-00020717.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Friede M, Mason S, Turnell WG, Vinals Y Bassolsc;  
XX  
XX WPI; 2002-489648/52.  
XX  
XX Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.

PS Claim 4; Page 9; 45pp; English.  
XX  
XX The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
CC immunogenic carrier. The vaccine can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (Ige) suitable to be cyclised and used in the invention  
XX  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 47; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQVMDVD 9  
|||  
2 EDGQVMDVD 10  
Db

RESULT 10  
ADE10902  
ID ADE10902 standard; peptide; 10 AA.  
XX  
AC ADE10902;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX Chimeric hepatitis B virus related B-cell epitope segid 136.  
XX  
DE  
XX hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;  
KW recombinant hepatitis B core chimeric protein; Hbc chimeric protein;  
KW hepatitis B infection; T-cell stimulator; B-cell epitope.  
XX  
XX Homo sapiens.  
XX  
XX US2003198645-A1.  
XX  
XX 23-OCT-2003.  
XX  
XX 21-FEB-2003; 2003US-00372076.  
XX  
XX 21-FEB-2002; 2002US-00080299.  
XX  
XX 21-FEB-2002; 2002US-00082014.  
XX  
XX (PAGE//) PAGE M.  
XX  
XX (FRIE//) FRIEDE M.  
XX  
XX Page M, Friede M;  
XX  
XX WPI; 2003-852775/79.  
XX  
XX Treating chronic hepatitis B infection by administering a T cell-  
PT stimulating vaccine containing immunogenic particles having recombinant  
PT carboxy-terminal truncated hepatitis B core (Hbc) chimeric protein  
PT molecules.  
XX  
XX disclosure; SEQ ID NO 136; 11pp; English.  
XX  
XX  
XX The invention describes a method of treating chronic hepatitis comprising  
CC administering to a patient a T cell-stimulating amount of a vaccine  
CC comprising immunogenic particles dissolved or dispersed in a diluent,  
CC where the immunogenic particles consists of recombinant hepatitis B core  
CC (Hbc) chimeric protein molecules, and maintaining the patient to induce T  
CC cells activated against Hbc. The methods and compositions of the present  
CC invention are useful for treating chronic hepatitis B infection. This is  
CC the amino acid sequence of a chimeric hepatitis B virus related B-cell  
CC epitope useful for expression within the HBV chimera at the N-terminus,  
CC within the immunogenic loop and/or at the C-terminus.  
XX  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 100.0%; Score 47; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
2 EDGQVMDVD 10

Db

RESULT 11  
AAB25916  
ID AAB25916 standard; peptide; 13 AA.  
XX  
AC AAB25916;  
XX  
DT 05-JAN-2001 (first entry)  
XX  
DE P1 mimotope peptide P15 SEQ ID NO:10.  
XX  
KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
allergic disease; immunophylaxis; immunotherapy; antiallergic;  
immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
allergy; atopy.  
XX  
OS Homo sapiens.  
XX  
PN WO200050460-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-EP001455.  
XX  
PR 25-FEB-1999; 99GB-00004405.  
PR 29-MAR-1999; 99GB-00007151.  
PR 07-MAY-1999; 99GB-00010537.  
PR 07-MAY-1999; 99GB-00010538.  
PR 07-AUG-1999; 99GB-00018594.  
PR 07-AUG-1999; 99GB-00018603.  
PR 07-SEP-1999; 99GB-00021046.  
PR 07-SEP-1999; 99GB-00021047.  
PR 29-OCT-1999; 99GB-00025619.  
PR 23-NOV-1999; 99GB-00027696.  
XX  
PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
(PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De BassolsC;  
XX  
DR MPI; 2000-572073/53.  
XX  
PT Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.  
XX  
PS Disclosure; Page 9; 129pp; English.

The present invention describes a peptide (I) comprising an isolated  
surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
for treating allergies comprising (II); (3) a ligand (IV) capable of  
recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
(5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
(IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can  
have antiallergic and immunosuppressive activities, and can be used as a  
vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
in medicine and in the manufacture of medicaments for treating and  
preventing allergies. (IV) is useful for identifying mimotopes of P1, in  
medicine and also in manufacturing medicaments for treating allergies.  
(I) is useful in diagnostics and in the affinity purification of  
circulating anti-IgE antibodies from blood. (I), (II) and PC are useful  
for treating a patient susceptible to or suffering from allergies. (IV)  
is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
peptide sequences which are used in the exemplification of the present

CC invention  
XX  
SQ Sequence 13 AA;

Query Match 100.0%; Score 47; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
2 EDGQVMDVD 11

Db

RESULT 12  
AAB25914  
ID AAB25914 standard; peptide; 13 AA.  
XX  
AC AAB25914;  
XX  
DT 05-JAN-2001 (first entry)  
XX  
DE P1 mimotope peptide P15 SEQ ID NO:8.  
XX  
KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
allergic disease; immunophylaxis; immunotherapy; antiallergic;  
immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
allergy; atopy.  
XX  
OS Homo sapiens.  
XX  
PN WO200050460-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 22-FEB-2000; 2000WO-EP001455.  
XX  
PR 25-FEB-1999; 99GB-00004405.  
PR 29-MAR-1999; 99GB-00007151.  
PR 07-MAY-1999; 99GB-00010537.  
PR 07-MAY-1999; 99GB-00010538.  
PR 07-AUG-1999; 99GB-00018594.  
PR 07-AUG-1999; 99GB-00018603.  
PR 07-SEP-1999; 99GB-00021046.  
PR 07-SEP-1999; 99GB-00021047.  
PR 29-OCT-1999; 99GB-00025619.  
PR 23-NOV-1999; 99GB-00027696.  
XX  
PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
(PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De BassolsC;  
XX  
DR MPI; 2000-572073/53.  
XX  
PT Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.  
XX  
PS Claim 14; Page 9; 129pp; English.

The present invention describes a peptide (I) comprising an isolated  
surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
for treating allergies comprising (II); (3) a ligand (IV) capable of  
recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
(5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
(IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can  
have antiallergic and immunosuppressive activities, and can be used as a  
vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
in medicine and in the manufacture of medicaments for treating and  
preventing allergies. (IV) is useful for identifying mimotopes of P1, in



CC protein D or its fragment; and (3) preparation of a vaccine of (1),  
 CC comprising formulating (1) with an excipient. (1) has cytostatic, (1)  
 CC antiallergic, neurotropic, neuroprotective and protozoacide activities. (1)  
 CC and the vaccine are useful for the manufacture of a medicament for  
 CC preventing and treating infectious diseases such as malaria or chronic  
 CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
 CC Unlike prior art immunogens, (1) induces high levels of antipeptide  
 CC immune responses while inducing a moderate humoral response against the  
 CC carrier. The present sequence represents a specifically claimed mimotope  
 CC peptide sequence, which can be used in an immunogen of the present  
 CC invention  
 XX

XX Sequence 13 AA;

Query Match 100.0%; Score 47; DB 3; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
 |||||  
 Db 3 EDGQVMDVD 11

RESULT 15

AAB51028  
 ID AAB51028 standard; peptide; 13 AA.

XX AC AAB51028;

XX DT 21-MAR-2001 (first entry)

XX DE IGE peptide #6.

XX KW Vaccine; immunoglobulin E; IGE; anti-allergy.

XX OS Mammalia.

XX PN WO200074716-A2.

XX PD 14-DEC-2000.

XX PF 06-JUN-2000; 2000WO-EP005164.

XX PR 08-JUN-1999; 99GB-00013327.

XX PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Prieels J;

XX DR WPI; 2001-091150/10.

PT New vaccine comprising allergy peptides linked by an inert carrier,  
 PT useful for boosting an anti-allergy immune response in an individual  
 PT susceptible to an allergic response.

PS Claim 5; Page 20; 26pp; English.

XX The present invention relates to a composition comprising allergy  
 CC peptides linked by an inert carrier. The allergy peptides are derived  
 CC from immunoglobulin E (IGE) or IGE receptor. The present peptide is one  
 CC such peptide from IGE. The composition is useful as a vaccine or for  
 CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
 CC In particular, for boosting an anti-allergy immune response in an  
 CC individual susceptible to an allergic response  
 XX

XX Sequence 13 AA;

Query Match 100.0%; Score 47; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
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Db 3 EDGQVMDVD 11

Search completed: August 23, 2004, 10:37:22  
 Job time : 125 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2004, 10:37:59 ; Search time 123 Seconds

(without alignments)  
22.994 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDGQVMDVD 9

Scoring table:

BIOSDM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 31425056 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubppaa/PCRUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	47	100.0	9	12 US-10-362-527-1	Sequence 1, Appli
2	47	100.0	9	14 US-10-082-014-273	Sequence 273, App
3	47	100.0	9	14 US-10-372-076-127	Sequence 127, App
4	47	100.0	9	16 US-10-677-074-127	Sequence 127, App
5	47	100.0	10	12 US-10-362-527-12	Sequence 12, Appl
6	47	100.0	10	14 US-10-082-014-282	Sequence 282, App
7	47	100.0	10	14 US-10-372-076-136	Sequence 136, App
8	47	100.0	10	14 US-10-677-074-136	Sequence 136, App
9	47	100.0	13	12 US-10-362-527-8	Sequence 8, Appli
10	47	100.0	13	12 US-10-362-527-10	Sequence 10, Appl
11	47	100.0	13	12 US-10-362-527-96	Sequence 96, Appl
12	47	100.0	14	12 US-10-362-527-324	Sequence 324, App
13	47	100.0	16	12 US-10-362-527-326	Sequence 326, App
14	47	100.0	20	12 US-10-362-527-100	Sequence 100, App
15	47	100.0	20	12 US-10-362-527-142	Sequence 142, App

16	47	100.0	20	12 US-10-362-527-328	Sequence 328, App
17	47	100.0	21	12 US-10-362-527-101	Sequence 101, App
18	47	100.0	21	12 US-10-362-527-143	Sequence 143, App
19	47	100.0	22	12 US-10-362-527-99	Sequence 99, Appl
20	47	100.0	22	12 US-10-362-527-327	Sequence 327, App
21	47	100.0	128	14 US-10-152-190-7	Sequence 7, Appli
22	47	100.0	236	14 US-10-152-190-9	Sequence 9, Appli
23	47	100.0	320	10 US-09-847-208-6	Sequence 6, Appli
24	47	100.0	320	12 US-10-000-439-6	Sequence 6, Appli
25	47	100.0	323	9 US-09-949-375A-2	Sequence 2, Appli
26	47	100.0	323	9 US-09-949-375A-4	Sequence 4, Appli
27	47	100.0	323	9 US-09-949-375A-6	Sequence 6, Appli
28	47	100.0	323	16 US-10-363-954A-2	Sequence 2, Appli
29	47	100.0	323	16 US-10-363-954A-4	Sequence 4, Appli
30	47	100.0	323	16 US-10-363-954A-6	Sequence 6, Appli
31	47	100.0	330	9 US-09-949-375A-10	Sequence 10, Appl
32	47	100.0	330	16 US-10-363-954A-10	Sequence 10, Appl
33	47	100.0	331	9 US-09-401-636-1	Sequence 1, Appli
34	47	100.0	331	14 US-10-176-664-1	Sequence 1, Appli
35	47	100.0	331	14 US-10-207-655-329	Sequence 329, App
36	47	100.0	331	16 US-10-673-594-1	Sequence 1, Appli
37	47	100.0	336	9 US-09-949-375A-8	Sequence 8, Appli
38	47	100.0	336	16 US-10-363-954A-8	Sequence 8, Appli
39	47	100.0	346	14 US-10-152-190-10	Sequence 10, Appl
40	47	100.0	346	14 US-10-152-190-14	Sequence 14, Appl
41	47	100.0	347	14 US-10-152-190-12	Sequence 12, Appl
42	47	100.0	347	14 US-10-152-190-13	Sequence 13, Appl
43	47	100.0	348	14 US-10-152-190-11	Sequence 11, Appl
44	47	100.0	426	14 US-10-214-524-26	Sequence 26, Appl
45	47	100.0	427	10 US-09-847-208-5	Sequence 5, Appli

#### ALIGNMENTS

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RESULT 1
US-10-362-527-1
; Sequence 1, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Tunell, William Gordon
; APPLICANT: Vinals y De Bassols, Carlota
; TITLE OR INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cycliced Peptide
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-1

Query Match      100.0%; Score 47; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 EDGQVMDVD 9

RESULT 2  
US-10-082-014-273  
; Sequence 273, Application US/10082014

```
Publication No. US2003018585A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.1
SEQ ID NO 273
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-082-014-273

Query Match
100.0%; Score 47; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 1 EDGQVMDVD 9

RESULT 3
US-10-372-076-127
Sequence 127, Application US/10372076
Publication No. US20030198645A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/372,076
PRIOR FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.2
SEQ ID NO 127
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-372-076-127

Query Match
100.0%; Score 47; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 1 EDGQVMDVD 9

RESULT 4
US-10-677-074-127
Sequence 127, Application US/10677074
Publication No. US20040156863A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Schmidt, Annette Elisabeth
APPLICANT: Stober, Detlef
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/677,074
CURRENT FILING DATE: 2003-10-01
```

```
PRIOR APPLICATION NUMBER: 10/372,076
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.2
SEQ ID NO 127
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-677-074-127

Query Match
100.0%; Score 47; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 1 EDGQVMDVD 9

RESULT 5
US-10-362-527-12
Sequence 12, Application US/10362527
Publication No. US20040030106A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnell, William Gordon
APPLICANT: Vinals Y De Baasols, Carlota
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
FILE REFERENCE: B45236
CURRENT APPLICATION NUMBER: US/10/362,527
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/EP01/09576
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: GB 0020717.5
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-362-527-12

Query Match
100.0%; Score 47; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
Db 2 EDGQVMDVD 10

RESULT 6
US-10-082-014-282
Sequence 282, Application US/10082014
Publication No. US2003018585A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.1
SEQ ID NO 282
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LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-082-014-282

Query Match 100.0%; Score 47; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 2 EDGQVMDVD 10

RESULT 7  
US-10-372-076-136

Sequence 136, Application US/10372076  
Publication No. US20030198645A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Mark  
APPLICANT: Page, Mark  
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 136  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-372-076-136

Query Match 100.0%; Score 47; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 2 EDGQVMDVD 10

RESULT 8  
US-10-677-074-136

Sequence 136, Application US/10677074  
Publication No. US20040156863A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Mark  
APPLICANT: Friede, Martin  
APPLICANT: Schmidt, Annette Elisabeth  
APPLICANT: Steber, Detlef  
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/677,074  
PRIOR FILING DATE: 2003-10-01  
PRIOR APPLICATION NUMBER: 10/372,076  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 136  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-677-074-136

Query Match 100.0%; Score 47; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 2 EDGQVMDVD 10

RESULT 9  
US-10-362-527-8

Sequence 8, Application US/10362527  
Publication No. US20040030106A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
APPLICANT: Vinals y De Bassols, Carlota  
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
FILE REFERENCE: B45236  
CURRENT APPLICATION NUMBER: US/10/362,527  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: PCT/EP01/09576  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: GB 0020717.5  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-362-527-8

Query Match 100.0%; Score 47; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 3 EDGQVMDVD 11

RESULT 10  
US-10-362-527-10

Sequence 10, Application US/10362527  
Publication No. US20040030106A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
APPLICANT: Vinals y De Bassols, Carlota  
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
FILE REFERENCE: B45236  
CURRENT APPLICATION NUMBER: US/10/362,527  
PRIOR FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: PCT/EP01/09576  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: GB 0020717.5  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-362-527-10

Query Match 100.0%; Score 47; DB 12; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9  
Db 3 EDQVMDVD 11

## RESULT 11

US-10-362-527-96  
; Sequence 96, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide  
US-10-362-527-96

Query Match 100.0%; Score 47; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9  
Db 3 EDQVMDVD 11

## RESULT 12

US-10-362-527-324  
; Sequence 324, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 324  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide  
US-10-362-527-324

Query Match 100.0%; Score 47; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.035;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9  
Db 5 EDQVMDVD 13

## RESULT 13

US-10-362-527-326  
; Sequence 326, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 326  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide  
US-10-362-527-326

Query Match 100.0%; Score 47; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9  
Db 3 EDQVMDVD 11

## RESULT 14

US-10-362-527-100  
; Sequence 100, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide  
US-10-362-527-100



Query Match 100.0%; Score 47; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
 |||||  
 Db 3 EDGQVMDVD 11

RESULT 15

US-10-362-527-142  
 ; Sequence 142, Application US/10362527  
 ; Publication No. US20040030106A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Friede, Martin  
 ; APPLICANT: Mason, Sean  
 ; APPLICANT: Turnell, William Gordon  
 ; APPLICANT: Vinals y De Bassols, Carlotia  
 ; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
 ; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
 ; FILE REFERENCE: B45236  
 ; CURRENT APPLICATION NUMBER: US/10/362,527  
 ; CURRENT FILING DATE: 2003-02-21  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
 ; PRIOR FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: GB 0020717.5  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 328  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 142  
 ; LENGTH: 20  
 ; TYPE: PRT  
 ; FEATURE:  
 ; ORGANISM: Artificial Sequence  
 ; OTHER INFORMATION: Artificial variant of Homo sapiens Igr peptide  
 ; US-10-362-527-142

Query Match 100.0%; Score 47; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
 |||||  
 Db 3 EDGQVMDVD 11

Search completed: August 23, 2004, 10:50:19  
 Job time : 124 secs

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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:35:24 ; Search time 32 Seconds

(Without alignments)  
14.520 Million cell updates/sec

Title: US-09-914-088-1  
Sequence: 1 EDGQVMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	74.5	1095	4 US-09-543-681A-6594	Sequence 6594, Ap
2	33	70.2	462	4 US-09-328-352-7128	Sequence 7128, Ap
3	33	70.2	468	4 US-09-252-991A-117208	Sequence 117208, A
4	33	70.2	948	4 US-09-328-352-6123	Sequence 6123, Ap
5	33	70.2	1119	3 US-09-386-651B-2	Sequence 2, Appl1
6	32	68.1	138	4 US-09-621-976-5032	Sequence 5032, Ap
7	32	68.1	273	4 US-09-427-700-12	Sequence 12, Appl1
8	32	68.1	293	4 US-09-252-991A-22215	Sequence 22215, A
9	32	68.1	394	3 US-08-705-771-21	Sequence 21, Appl1
10	32	68.1	422	1 US-09-417-540-21	Sequence 21, Appl1
11	32	68.1	422	1 US-08-152-483B-3	Sequence 3, Appl1
12	32	68.1	426	1 US-08-152-483B-7	Sequence 7, Appl1
13	32	68.1	478	1 US-08-152-483B-9	Sequence 9, Appl1
14	32	68.1	508	2 US-08-724-281-1	Sequence 1, Appl1
15	32	68.1	508	4 US-09-134-377-1	Sequence 1, Appl1
16	32	68.1	1357	4 US-09-252-991A-21308	Sequence 21308, A
17	32	68.1	1655	4 US-09-866-108A-15753	Sequence 15753, A
18	31.5	67.0	90	4 US-09-227-357-635	Sequence 635, App
19	31.5	67.0	232	2 US-08-773-910-1	Sequence 1, Appl1
20	31.5	67.0	232	4 US-09-199-892-1	Sequence 1, Appl1
21	31	66.0	160	1 US-08-441-629-7	Sequence 7, Appl1
22	31	66.0	160	4 US-08-776-207-7	Sequence 7, Appl1
23	31	66.0	160	4 US-09-507-773-7	Sequence 7, Appl1
24	31	66.0	160	5 PCT-US95-09172-7	Sequence 7, Appl1
25	31	66.0	181	4 US-09-489-039A-9676	Sequence 9676, Ap
26	31	66.0	247	4 US-09-452-239-44	Sequence 44, Appl1
27	31	66.0	294	4 US-09-252-991A-22068	Sequence 22068, A

28	31	66.0	294	4 US-09-198-452A-1081	Sequence 1081, Ap
29	31	66.0	303	4 US-09-107-532A-6113	Sequence 6113, Ap
30	31	66.0	332	4 US-09-134-001C-3199	Sequence 3199, Ap
31	31	66.0	410	4 US-09-252-991A-22340	Sequence 22340, A
32	31	66.0	411	2 US-08-933-115-2	Sequence 2, Appl1
33	31	66.0	411	3 US-09-205-008-2	Sequence 2, Appl1
34	31	66.0	411	4 US-09-206-115-2	Sequence 2, Appl1
35	31	66.0	473	4 US-09-107-532A-7057	Sequence 7057, Ap
36	31	66.0	517	4 US-09-489-039A-9854	Sequence 9854, Ap
37	31	66.0	520	4 US-09-252-991A-31115	Sequence 31115, A
38	31	66.0	520	2 US-09-091-432-2	Sequence 2, Appl1
39	31	66.0	520	4 US-09-387-663-2	Sequence 4, Appl1
40	31	66.0	520	4 US-09-214-139B-4	Sequence 4, Appl1
41	31	66.0	604	4 US-09-328-352-6437	Sequence 6437, Ap
42	31	66.0	735	4 US-09-134-001C-3440	Sequence 3440, Ap
43	31	66.0	802	4 US-09-489-039A-11230	Sequence 11230, A
44	30	63.8	29	4 US-09-849-039A-164A-6	Sequence 6, Appl1
45	30	63.8	52	4 US-09-621-976-6581	Sequence 6581, Ap

## ALIGNMENTS

RESULT 1  
US-09-543-681A-6594  
Sequence 6594, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETTON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709, 1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 6594  
LENGTH: 1095  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-6594

Query Match 74.5% ; Score 35; DB 4; Length 1095;  
Best local Similarity 77.8% ; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 139 EKGQVMDVD 147  
US-09-328-352-7128  
Sequence 7128, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7128  
LENGTH: 462  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7128

Query Match 70.2% ; Score 33; DB 4; Length 462;  
Best local Similarity 85.7% ; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMDVD 9  
||:||||  
Db 188 GQVMDVD 194

RESULT 3  
US-09-252-991A-17208  
; Sequence 17208, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17208  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17208

Query Match 70.2%; Score 33; DB 4; Length 468;  
Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMDVD 9  
||:||||  
Db 194 GQVMDVD 200

RESULT 4  
US-09-328-352-6123  
; Sequence 6123, Application US/09328352  
; Patent No. 6562938  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 6123  
; LENGTH: 948  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-6123

Query Match 70.2%; Score 33; DB 4; Length 948;  
Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQVMDVD 9  
||:||||  
Db 186 DQVMDVD 193

RESULT 5  
US-09-396-651B-2  
; Sequence 2, Application US/09396651B  
; Patent No. 6225076  
; GENERAL INFORMATION:  
; APPLICANT: Darst, Seth A  
; APPLICANT: Zhang, Gongyi  
; APPLICANT: Campbell, Elizabeth  
; APPLICANT: Minakin, Leonid

; APPLICANT: Severinov, Konstantin  
; TITLE OF INVENTION: A CRYSTAL OF BACTERIAL CORE RNA POLYMERASE AND METHODS  
; TITLE OF INVENTION: OR USE THEREOF  
; FILE REFERENCE: 600-1-258  
; CURRENT APPLICATION NUMBER: US/09/396,651B  
; CURRENT FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1119  
; TYPE: PRT  
; ORGANISM: Thermus aquaticus  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (695)..(696)  
; OTHER INFORMATION: Any amino acids can be at these two positions.  
US-09-396-651B-2

Query Match 70.2%; Score 33; DB 3; Length 1119;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9  
||:||||  
Db 599 EDQVMDVD 607

RESULT 6  
US-09-621-976-5032  
; Sequence 5032, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5032  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-621-976-5032

Query Match 68.1%; Score 32; DB 4; Length 138;  
Best Local Similarity 66.7%; Pred. No. 55;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDQVMDVD 9  
||:||||  
Db 115 EDQVMDVD 123

RESULT 7  
US-09-427-700-12  
; Sequence 12, Application US/09427700  
; Patent No. 6372489  
; GENERAL INFORMATION:  
; APPLICANT: AntiCancer  
; APPLICANT: Zhao, Ming  
; TITLE OF INVENTION: METHOD AND MODEL FOR HAIR PIGMENTATION  
; FILE REFERENCE: 31276-20017.00  
; CURRENT APPLICATION NUMBER: US/09/427,700  
; CURRENT FILING DATE: 1999-10-27  
; PRIOR APPLICATION NUMBER: US 60/105,725  
; PRIOR FILING DATE: 1998-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 273

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Deduced amino acid sequence of SEQ ID NO:11  
US-09-427-700-12

Query Match 68.1%; Score 32; DB 4; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGYMD 7  
Db 112 DQGYMD 117

RESULT 8  
US-09-252-991A-22215  
Sequence 22215, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: MARC J. RUBENFIELD et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22215  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22215

Query Match 68.1%; Score 32; DB 4; Length 293;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 233 EDAEVADVD 241

RESULT 9  
US-08-705-771-21  
Sequence 21, Application US/08705771  
Patent No. 6054289  
GENERAL INFORMATION:  
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,  
APPLICANT: Jian Ni and Jing-Shan Hu  
TITLE OF INVENTION: Human Genes, Sequences and  
TITLE OF INVENTION: Expression Products  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,771  
FILING DATE: August 30, 1996  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-705-771-21

Query Match 68.1%; Score 32; DB 3; Length 394;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 9 EDGLSDSD 17

RESULT 10  
US-09-417-540-21  
Sequence 21, Application US/09417540  
Patent No. 6639052  
GENERAL INFORMATION:  
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,  
APPLICANT: Jian Ni and Jing-Shan Hu  
TITLE OF INVENTION: Human Genes, Sequences and  
CORRESPONDENCE ADDRESS: Expression Products  
ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/417,540  
FILING DATE: 14-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/705,771  
FILING DATE: August 30, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 973-994-1700  
TELEFAX: 973-994-1744  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-417-540-21

Query Match 68.1%; Score 32; DB 4; Length 394;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
Db 9 EDGQISDSD 17

RESULT 11  
US-08-152-483B-3  
Sequence 3, Application US/08152483B  
Patent No. 552909

GENERAL INFORMATION:  
APPLICANT: Della-Cioppa, Guy  
TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 2730 Sand Hill Road  
CITY: Menlo Park  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,483B  
FILING DATE: No. 552909 September 12, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 7/857,602  
FILING DATE: March 30, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 923,692  
FILING DATE: July 31, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 600,244  
FILING DATE: October 22, 1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 641,617  
FILING DATE: January 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 737,899  
FILING DATE: July 26, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: BIOG-20240/8129-040  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 422  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM:  
IMMEDIATE SOURCE:  
CLONE:  
FEATURE:  
US-08-152-483B-3

Query Match 68.1%; Score 32; DB 1; Length 422;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQVMD 7  
Db 112 DGQVMD 117

RESULT 12  
US-08-152-483B-7  
Sequence 7, Application US/08152483B  
Patent No. 552909

GENERAL INFORMATION:  
APPLICANT: Della-Cioppa, Guy  
TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 2730 Sand Hill Road  
CITY: Menlo Park  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,483B  
FILING DATE: No. 552909 September 12, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 7/857,602  
FILING DATE: March 30, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 923,692  
FILING DATE: July 31, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 600,244  
FILING DATE: October 22, 1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 641,617  
FILING DATE: January 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 737,899  
FILING DATE: July 26, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: BIOG-20240/8129-040  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: circular  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM:  
IMMEDIATE SOURCE:  
CLONE:

FEATURE:  
US-08-152-483B-7  
Query Match 68.1%; Score 32; DB 1; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DQGYMD 7  
Db 264 DQGYMD 269  
RESULT 13  
US-08-152-483B-9  
Sequence 9, Application US/08152483B  
Patent No. 5529909  
GENERAL INFORMATION:  
APPLICANT: Della-Cioppa, Guy  
APPLICANT: Kumagai, Monte  
TITLE OF INVENTION: TYROSINASE-ACTIVATOR  
TITLE OF INVENTION: PROTEIN FUSION ENZYME  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 2730 Sand Hill Road  
CITY: Menlo Park  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0,  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,483B  
FILING DATE: No. 5529909 September 12, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 7/857,602  
FILING DATE: March 30, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 923,692  
FILING DATE: July 31, 1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 600,244  
FILING DATE: October 22, 1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 641,617  
FILING DATE: January 16, 1991  
PRIOR APPLICATION DATA: 737,899  
FILING DATE: July 26, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: BIOC-20240/8129-040  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-3660  
TELEFAX: (415) 854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
DESCRIPTION: NO  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

ORGANISM:  
IMMEDIATE SOURCE:  
CLONE:  
FEATURE:  
US-08-152-483B-9  
Query Match 68.1%; Score 32; DB 1; Length 478;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DQGYMD 7  
Db 316 DQGYMD 321  
RESULT 14  
US-08-724-281-1  
Sequence 1, Application US/08724281  
Patent No. 5874089  
GENERAL INFORMATION:  
APPLICANT: SCHLEGEL, C. Richard  
APPLICANT: JENSON, A. Bennett  
APPLICANT: GHIM, Shin-Je  
TITLE OF INVENTION: PAPILOMAVIRUS VACCINES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,281  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,691  
FILING DATE: 02-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 010091-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 508 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-724-281-1  
Query Match 68.1%; Score 32; DB 2; Length 508;  
Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EDQGYMDV 8  
Db 200 EDQGYMDI 207  
RESULT 15  
US-09-134-377-1  
Sequence 1, Application US/09134377  
Patent No. 6485728

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; GENERAL INFORMATION:
; APPLICANT: SCHLEGEL, C. Richard
; APPLICANT: JENSON, A. Bennett
; APPLICANT: GHIM, Shin-Je
; TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/724,281
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 010091-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 508 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-09-134-377-1
;
Query Match 68.1%; Score 32; DB 4; Length 508;
Best local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDGQVMDV 8
Db 200 EDGDMMDI 207
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Search completed: August 23, 2004, 10:41:13  
Job time : 34 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:50:26 ; Search time 37 Seconds

(without alignments)  
23.398 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQVMDVD 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	36.2	6	2	PT0604
2	17	36.2	6	2	PT0657
3	17	36.2	7	2	PT0543
4	17	36.2	8	2	A28719
5	16	34.0	9	2	A37027
6	16	34.0	9	2	A60427
7	14	29.8	4	2	PT0271
8	14	29.8	7	2	S29735
9	14	29.8	8	2	PT0557
10	14	29.8	9	2	B39841
11	14	29.8	9	2	D44787
12	13	29.8	9	2	A56029
13	13	27.7	4	2	A41890
14	13	27.7	6	2	B35640
15	13	27.7	7	2	PC2370
16	13	27.7	8	2	PT0279
17	13	27.7	8	2	S66296
18	13	27.7	9	2	B45796
19	13	27.7	9	2	A61230
20	13	27.7	9	2	D48186
21	13	27.7	9	2	C60070
22	12	25.5	5	2	B31836
23	12	25.5	5	2	PT0699
24	12	25.5	5	2	PT0703
25	12	25.5	6	2	PC4392
26	12	25.5	6	2	A20186
27	12	25.5	6	2	PT0720
28	12	25.5	6	2	PT0589
29	12	25.5	7	2	S20446

30	12	25.5	7	2	B39127	phosphotransferase
31	12	25.5	7	2	PT0611	T-cell receptor be
32	12	25.5	7	2	PT0523	T-cell receptor be
33	12	25.5	7	2	PT0665	T-cell receptor be
34	12	25.5	7	2	PT0567	T-cell receptor be
35	12	25.5	7	2	PT0689	T-cell receptor be
36	12	25.5	7	2	PT0688	T-cell receptor be
37	12	25.5	8	2	B60588	sperm-activating p
38	12	25.5	8	2	G60588	urine glycopeptide
39	12	25.5	8	2	XGHUVU	Ig heavy chain CRD
40	12	25.5	8	2	PT0298	T-cell receptor be
41	12	25.5	8	2	PT0613	T-cell receptor be
42	12	25.5	8	2	PT0547	T-cell receptor be
43	12	25.5	8	2	PT0724	T-cell receptor be
44	12	25.5	8	2	PT0725	T-cell receptor be
45	12	25.5	8	2	A25836	L-serine ammonia-1

#### ALIGNMENTS

RESULT 1  
PT0604  
T-cell receptor beta chain V-D-J region (111-1A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0604  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0604  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEBS>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQ 4  
DB 4 DGQ 6

RESULT 2  
PT0657  
T-cell receptor beta chain V-D-J region (121-1K) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0657  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0657  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEBS>  
A:Experimental source: day 4 postnatal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQ 4  
DB 4 DGQ 6

## RESULT 3

PT0543  
T-cell receptor beta chain V-D-J region (126-186) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PT0543  
R/Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A/Reference number: PT0509; MUID:91277601; PMID:1711558  
A/Accession: PT0543  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-7 <FEE>  
A/Experimental source: day 18 fetal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 36.2%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQ 4  
|||  
Db 4 DQ 6

## RESULT 4

A28719  
thymic humoral factor gamma-2 - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1993  
C/Accession: A28719  
R/Burstein, Y.; Buchner, V.; Becht, M.; Trainin, N.  
Biochemistry 27, 4066-4071, 1988  
A/Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immun  
A/Reference number: A28719; MUID:88326920; PMID:3261994  
A/Accession: A28719  
A/Molecule type: protein  
A/Residues: 1-8 <BDR>

Query Match 36.2%; Score 17; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3  
|||  
Db 2 EDG 4

## RESULT 5

A37027  
macrophage chemotactic factor - human (fragment)  
N/Alternate names: T-cell hybridoma D6-18 protein  
C/Species: Homo sapiens (man)  
C/Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 23-Feb-1997  
C/Accession: A37027  
R/Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.  
Cell. Immunol. 123, 212-225, 1989  
A/Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.  
A/Reference number: A37027; MUID:89376581; PMID:2505934  
A/Accession: A37027  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <YOS>

Query Match 34.0%; Score 16; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3  
|||  
Db 5 ZDG 7

## RESULT 6

A60427  
macrophage cytotoxicity-inducing factor, 29K - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 18-Jun-1993  
C/Accession: A60427  
R/Jones, C.M.; Prince, C.A.; Williams, J.S.  
Exp. Hematol. 19, 704-709, 1991  
A/Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducing  
A/Reference number: A60427; MUID:91372335; PMID:1909970  
A/Accession: A60427  
A/Molecule type: protein  
A/Residues: 1-9 <JON>  
A/Note: the sequence from the text on page 706 is inconsistent with that from page 708 in  
C/Keywords: cytokine

Query Match 34.0%; Score 16; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDG 4  
|||  
Db 6 EDSQ 9

## RESULT 7

PT0271  
Ig heavy chain CRD3 region (clone 3-103A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0271  
R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j c  
A/Reference number: PT0222; MUID:91108357; PMID:1899102  
A/Accession: PT0271  
A/Molecule type: DNA  
A/Residues: 1-4 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotrimer; immunoglobulin

Query Match 29.8%; Score 14; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DQ 5  
|||  
Db 1 DQ 4

## RESULT 8

S29735  
polysphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi;  
C/Species: Propionibacterium freudenreichi subsp. shermanii  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
C/Accession: S29735  
R/Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A/Title: The polysphosphate- and ATP-dependent glucokinase from Propionibacterium shermani  
A/Reference number: S29735; MUID:93143332; PMID:8380966  
A/Accession: S29735  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <PHI>  
C/Keywords: phosphotransferase

Query Match 29.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 VMDVD 9  
|||

Db 3 VLGID 7

## RESULT 9

PT0557  
T-cell receptor beta chain V-D-J region (126-1BD) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PT0557  
R/Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A/Reference number: PT0509; MUID:91277601; PMID:1711558  
A/Accession: PT0557  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-8 <PEE>  
A/Experimental source: day 18 fetal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 29.8%; Score 14; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3  
|||  
Db 4 DDG 6

## RESULT 10

B39841  
dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)  
C/Species: Streptococcus sobrinus  
C/Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 23-Jun-1993  
C/Accession: B39841  
R/Mooser, G.; Hetta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.  
J. Biol. Chem. 266, 8916-8922, 1991  
A/Title: Isolation and sequence of an active-site peptide containing a catalytic aspartate  
A/Reference number: A39841; MUID:91224988; PMID:1827439  
A/Accession: B39841  
A/Status: Preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <MOO>  
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 29.8%; Score 14; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGGVMD 7  
|||  
Db 1 DGVVMD 6

## RESULT 11

D44787  
calliphoramide 13 - bluebottle fly (Calliphora vomitoria)  
C/Species: Calliphora vomitoria  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
C/Accession: D44787  
R/Duue, H.; Johansen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
A/Reference number: A41978; MUID:92196111; PMID:1549595  
A/Accession: D44787  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <DUV>  
C/Keywords: amidated carboxyl end; neuropeptide  
F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 29.8%; Score 14; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3  
|||  
Db 3 QDG 5

## RESULT 12

A56029  
N-methylpurine DNA glycosylase - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 19-Jan-1996  
C/Accession: A56029  
R/Roy, R.; Brooks, C.; Mitra, S.  
Biochemistry 33, 15131-15140, 1994  
A/Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA  
A/Reference number: A56029; MUID:95092772; PMID:7999773  
A/Accession: A56029  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <ROY>

Query Match 29.8%; Score 14; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQV 5  
|||  
Db 4 EVGQM 8

## RESULT 13

A41890  
protein D - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-Sep-1993  
C/Accession: A41890  
R/Stettan, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindqvist, B.H.  
J. Bacteriol. 174, 4094-4100, 1992  
A/Title: Escherichia coli K-12 and B contain functional bacteriophage P2 ogr genes.  
A/Reference number: A41890; MUID:92283767; PMID:1597424  
A/Accession: A41890  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-4 <SLR>  
A/Cross-references: GB:M81463

Query Match 27.7%; Score 13; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQ 4  
|||  
Db 1 EDNE 4

## RESULT 14

B35640  
cerebellar degeneration-related protein - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 24-Jun-1993  
C/Accession: B35640  
R/Chem, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990  
A/Title: Cerebellar degeneration-related antigen: a highly conserved neuroecodermal mar  
A/Reference number: A35640; MUID:90222173; PMID:2326268  
A/Accession: B35640  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-6 <CHE>

Query Match 27.7%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVD 9  
|:|

Db 4 DLD 6

## RESULT 15

PC2370

Probable H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain [similarity] - Bac

N;Alternate names: unidentified 78K protein

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 03-Jun-2002

C;Accession: PC2370

R;Matsumo, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation i

A;Reference number: PC2369; MUID:95218265; PMID:776022

A;Accession: PC2370

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <Mas>

C;Keywords: ATP biosynthesis; hydrolase

## Query Match

Best Local Similarity 27.7%; Score 13; DB 2; Length 7;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 MPVD 9  
|:|

Db 1 MDLN 4

Search completed: August 23, 2004, 10:56:40  
Job time : 38 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:41:20 ; Search time 22 Seconds

(without alignments)  
21,301 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQVMDVD 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	34.0	8	1	ACT_CARMA
2	16	34.0	8	1	PLP_BRANA
3	15	31.9	9	1	D1_NEPNO
4	14	29.8	9	1	FARD_CALVO
5	12	25.5	8	1	GLUR_HUMAN
6	12	25.5	9	1	FAR6_MARKS
7	12	25.5	9	1	IPYR_RHOVI
8	12	25.5	9	1	RE42_LITRU
9	12	25.5	9	1	UF02_MOUSE
10	11	23.4	6	1	ACPH_RABIT
11	11	23.4	7	1	BRHP_CONIM
12	11	23.4	7	1	FARS_HIRME
13	11	23.4	7	1	IGAO_DACDE
14	11	23.4	7	1	UH11_RAT
15	11	23.4	8	1	AL17_CARMA
16	11	23.4	8	1	CCKN_MACEU
17	11	23.4	8	1	WPL_PERRAT
18	11	23.4	9	1	AL11_CARMA
19	11	23.4	9	1	ALC_CHURE
20	11	23.4	9	1	FARS_CALVO
21	11	23.4	9	1	FAR6_CALVO
22	11	23.4	9	1	FAR7_CALVO
23	11	23.4	9	1	LPCA_STRAU
24	11	23.4	9	1	PPH1_LYCES
25	10	21.3	5	1	BIOA_CITFR
26	10	21.3	5	1	RE11_LITRU
27	10	21.3	6	1	CIP1_MYTED
28	10	21.3	7	1	UF03_MOUSE
29	10	21.3	8	1	CLP_THICU
30	10	21.3	8	1	UF06_MOUSE
31	10	21.3	9	1	FIBB_PAPNA
32	10	21.3	9	1	FIBB_PAPHA
33	10	21.3	9	1	FIBB_THERG

34	10	21.3	9	1	LITO_LITAU	P08945	litorea aur
35	10	21.3	9	1	LITR_PHYMO	P08946	phyllomedus
36	10	21.3	9	1	MOSF_CIXYA	P19853	clypeaster
37	10	21.3	9	1	MOSH_CIXYA	P19852	clypeaster
38	10	21.3	9	1	UHA2_HUMAN	P40929	homo sapien
39	10	21.3	9	1	UPA6_HUMAN	P30092	homo sapien
40	9	19.1	6	1	CIP2_MYTED	P13737	mytilus edu
41	9	19.1	7	1	WMA1_ACHFU	P35919	achatina fu
42	9	19.1	7	1	WMA2_ACHFU	P35920	achatina fu
43	9	19.1	7	1	WMA3_ACHFU	P35921	achatina fu
44	9	19.1	8	1	AKHG_GRYBI	P14086	grylus bim
45	9	19.1	8	1	AKH_LIBAU	P25418	libellula a

## ALIGNMENTS

RESULT 1  
ACT\_CARMA STANDARD; PRT; 8 AA.  
AC P80709;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Actin (Fragment).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxId=6759;  
RN [1]  
RP SEQUENCE.  
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
RA Baghdassarian D.;  
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";  
RL Endocrine 5:23-32(1996).  
CC -!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 6.8. ITS MW IS: 46 kDa.  
CC -!- SIMILARITY: Belongs to the actin family.  
DR InterPro: IPR004001; Actin.  
DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE: PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
KW Structural protein.  
FT NON TER 1 8  
FT NON TER 1 8  
SQ SEQUENCE 8 AA; 976 MW; 142405AB2CAEB3 CRC64;  
Query Match 34.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 DVD 9  
Db 3 DVD 5  
RESULT 2  
PLP\_BRANA STANDARD; PRT; 8 AA.  
ID PLP\_BRANA  
AC P81707;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Plasmidial lipid-associated protein (Fragment).  
OS Brassica napus (Rape).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OX	euroside II; Brassicales; Brassicaceae; Brassica.
RN	NCBI_TaxId=3708;
RN	[1]
RP	SEQUENCE.
RC	STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RC	MEDLINE=99349136; PubMed=10420651;
RA	Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA	Murphy D.J.;
RT	"Composition and role of tapetal lipid bodies in the biogenesis of the
RT	pollen coat of Brassica napus.";
RL	Planta 208:588-598(1999).
CC	-1- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC	specific plastidial lipid organelle.
CC	-1- TISSUE SPECIFICITY: Tapetum of anthers.
FT	NON TER
FT	8
FT	8
SQ	SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;
QY	Query Match 34.0%; Score 16; DB 1; Length 8;
Db	Best Local Similarity 60.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches	3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	5 VMDVD 9
Db	1 VIDVN 5
RESULT 3	
ID	D1_NEPNO STANDARD; PRT; 9 AA.
AC	P24816;
DT	01-MAR-1992 (Rel. 21, Created)
DT	01-MAR-1992 (Rel. 21, Last sequence update)
DT	01-MAR-1992 (Rel. 21, Last annotation update)
DE	Gastrin/cholecystokinin-like peptide D1.
OS	Nephraps norvegicus (Norway lobster).
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC	Nephropoidea; Nephropidae; Nephrops.
OX	NCBI_TaxId=6829;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Stomach;
RC	MEDLINE=92082847; PubMed=1747388;
RA	Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;
RT	"Structure and biological activity of crustacean gastrointestinal
RT	peptides identified with antibodies to gastrin/cholecystokinin.";
RL	Biochimie 73:1233-1239(1991).
CC	-1- FUNCTION: May control digestion processes in crustaceans.
CC	-1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC	PIR: S47432; S47432.
KW	Hormone.
SQ	SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;
QY	Query Match 31.9%; Score 15; DB 1; Length 9;
Db	Best Local Similarity 75.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 EDGQ 4
Db	2 EGQ 5
RESULT 4	
ID	FARD_CALVO STANDARD; PRT; 9 AA.
AC	P41868;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	01-NOV-1995 (Rel. 32, Last annotation update)
DE	CallipMERamide 13.
OS	Calliphora vomitoria (Blue blowfly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

CC	Calliphoridae; Calliphora.
OX	NCBI_TaxId=27454;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Thoracic ganglion;
RX	MEDLINE=2219611; Pubmed=1549595;
RA	Dave H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA	Rehfeld J.F., Thorpe A.;
RT	"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT	neuropeptides (designated calliphorFamides) from the blowfly
RT	Calliphora vomitoria.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC	-1- SMILIRITY: Belongs to the FARP (FMRFamide related peptide)
CC	family.
DR	PIR: D4787; D44787.
KW	Neuropeptide; Amidation.
FT	MOD RES 9
SEQUENCE	9 AA; 1028 MW; 22D10699C87ABD8 CRC64;
	AMIDATION.
Query Match	22.8%; Score 14; DB 1; Length 9;
Best Local Similarity	66.7%; Pred. No. 1.4e+05;
Matches	2; Conservative 1; Mismatches 0; Gaps 0;
QY	1 EDG 3
	:
Db	3 QDG 5

```

RESULT 5
GLUR_HUMAN
ID _GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126985;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25P-25P(1971).
CC -1- FUNCTION: The identity of the glycoprotein from which this peptide
CC is derived is unknown. No physiological function has been
CC attributed. An erythrocyte membrane glycopeptide having a
CC similar structure has also been found.
DR PIR; A03188; XGHUEU.
DR GO; GO:0005576; C:extracellular; NAS.
KW glycoprotein.
FT CARBOHYD
SQ SEQUENCE 8 AA; 855 MW; C2D87A1F5B1B1E CRC64;

Query Match 25.5%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DG 3
||
Db 6 DG 7

RESULT 6
FAR6_MACRS
FAR6_MACRS STANDARD; PRT; 9 AA.
AC P83279;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DE FMRFamide-like neuropeptide FLRP6 (DGRNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidae; Palaemonidae; Macrobrachium.  
 RX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21107394; PubMed=11179812;  
 RA Stihigorngul P., Saraihongkum W., Longyant S., Panchan N.,  
 RA Stihigorngul W., Peterson A.;  
 RT "Three more novel FMRFamide-like neuropeptide sequences from the  
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";  
 RL Peptides 22:191-197(2001).  
 CC -1- MASS SPECTROMETRY: MW=1080.7, METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 DR GO: GO:0007218; P:neuropeptide signaling pathway; IDA.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DG 3  
 Db 1 DG 2

RESULT 7  
 ID PYR\_RHOVI STANDARD; PRT; 9 AA.  
 AC P82932;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphatase phospho-  
 DE hydrolase) (Ppase) (Fragment).  
 GN PPA.  
 OS Rhodospirillum rubrum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Hyphomicrobiaceae; Blastochloris.  
 RX NCBI\_TaxID=1079;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.  
 RA Gomez R., Losada M., Serrano A.;  
 RL Submitted (JUN-2001) to Swiss-Prot.  
 CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS PROTEIN IS:  
 CC 23 KDa.  
 CC -1- SIMILARITY: Belongs to the Ppase family.  
 DR HAMAP: MF\_00209; -1.  
 DR InterPro: IPR008162; Pyrophosphatase.  
 DR PROSITE: PS00387; PPAse, PARTIAL.  
 KW Hydrolyase.  
 FT NON TER 9  
 FT NCBI\_TaxID=10090;  
 SQ SEQUENCE 9 AA; 1014 MW; 68F3EAA05DDAA044 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 MDVD 9  
 Db 1 WRID 4

RESULT 8  
 RE42\_LITRU

ID RE42\_LITRU STANDARD; PRT; 9 AA.  
 AC P82075; P82093;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 4.2/4.3.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 RX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-  
 CC terminal amidation.  
 CC -1- MASS SPECTROMETRY: MW=883; METHOD=FAB.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 9  
 FT NCBI\_TaxID=10090;  
 SQ SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;

Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 VMDV 8  
 Db 3 LIDI 6

RESULT 9  
 ID UF02\_MOUSE STANDARD; PRT; 9 AA.  
 AC P38640;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.0, its MW is: 32 kDa.  
 FT NON TER 9  
 FT NCBI\_TaxID=10090;  
 SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 25.5%; Score 12; DB 1; Length 9;  
 Best Local Similarity 16.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;  
 Matches 1; Conservative 3; Mismatches 2;

QY 2 DQVMD 7  
 2 EDELTD 7

RESULT 10

ACPH RABIT STANDARD; PRT; 6 AA.  
 AC P25154;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide hydrolase) (ABH) (Acylaminoacyl-peptidase) (Fragment).  
 GN APEH.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Muscle;  
 RX MEDLINE=92222120; PubMed=1807161;  
 RA Krishna R.G., Chin C.C.Q., Wolf F.;  
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after unblocking with N-acetylaminoacyl-peptide hydrolase."  
 RL Anal. Biochem. 199:45-50(1991).  
 CC -1- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal peptide bond of an N-acetylated peptide to generate an N-acetylated amino acid and a peptide with a free N-terminus. It preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.  
 CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid + peptide.  
 CC -1- SUBUNIT: Homotetramer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to peptidase family S9C.  
 DR PIR: A49792; A49792.  
 DR MEROPS: S09.004; -.  
 DR InterPro: IPR002471; Pept S9 AS.  
 DR PROSITE: PS00708; PRO\_ENDOPEP\_SER; PARTIAL.  
 KW Hydrolase; Acetylation.  
 FT MOD\_RES 1 ACETYLTATION.  
 FT NON\_TER 6  
 FT SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;  
 SQ

Query Match 23.4%; Score 11; DB 1; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 1; Mismatches 0;

QY 4 QVM 6  
 4 QVL 6

RESULT 11  
 BRHP CONIM STANDARD; PRT; 7 AA.  
 AC P58603;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bromoheptapeptide Im.  
 OS Conus imperialis (Imperial cone).  
 OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeconcha; Hypogastropoda;  
 OC Neogastropoda; Conidae; Conidae; Conus.  
 OX NCBI\_TaxID=35631;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=Venom;  
 RX MEDLINE=97184108; PubMed=9030520;  
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Guliyas J.,  
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
 RA McIntosh J.M.;  
 RT "A novel post-translational modification involving bromination of tryptophan. Identification of the residue, U-6-bromotryptophan, in peptides from Conus imperialis and Conus radiatus venom."  
 RL J. Biol. Chem. 272:4689-4698(1997).  
 CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSTMS.  
 DR PIR: A58512; A58512.  
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.  
 FT DISULFD 2 7  
 FT MOD\_RES 1 1  
 FT MOD\_RES 6 6  
 FT MOD\_RES 7 7  
 FT MOD\_RES 7 7  
 FT SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;  
 SQ

Query Match 23.4%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

QY 3 GQ 4  
 3 GQ 4

RESULT 12  
 FARS HIRME STANDARD; PRT; 7 AA.  
 ID FARS HIRME  
 AC P42564;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide GGRMP-amide.  
 OS Hirudo medicinalis (Medical leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudinae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsotis M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7  
 FT SEQUENCE 7 AA; 858 MW; 69D4068B5387810 CRC64;  
 SQ

Query Match 23.4%; Score 11; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 1; Mismatches 1;

QY 3 GQVM 6  
 2 GQVM 5

RESULT 13  
 IGAO DACDB STANDARD; PRT; 7 AA.  
 ID IGAO DACDB  
 AC P06294;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Galactose oxidase inhibitor.  
 OS Dactylium dendroides (Cladobotryum dendroides).



OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
 OX NCBI\_TaxID=5112;  
 RN [1]  
 RP SEQUENCE.  
 RA Avigad G., Markus Z.;  
 RT "Identification of a peptide inhibitor of galactose oxidase from  
 RL Dactylium dendroides";  
 RL Fed. Proc. 31:447-447(1972).  
 CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the  
 CC galactose oxidase apoenzyme. It may inactivate the enzyme by  
 CC binding to its prosthetic copper group.  
 CC PIR; A01341; XEYDGD.  
 DR Copper; Metalloenzyme inhibitor.  
 KW SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 23.4%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GQ 4  
 ||  
 2 GQ 3

Db

RESULT 14  
 ID UH11 RAT STANDARD; PRT; 7 AA.  
 AC P56576;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Schejter C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to Swiss-Prot.  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 8.5, its MW is: 42 kDa.  
 CC UNSURE 2 2 OR A.  
 FT NON TER 7 7  
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 23.4%; Score 11; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EDG 3  
 ||  
 5 EOG 7

Db

RESULT 15  
 ID AL17\_CARMA STANDARD; PRT; 8 AA.  
 AC P81820;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinus maenas (Common shore crab) (Green crab).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaro P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 CC Neuropeptide; Amidation; Multigene family.  
 KW MOD PSS 8 8 AMIDATION (POTENTIAL).  
 FT MOD PSS 8 8  
 SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match 23.4%; Score 11; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GQ 4  
 ||  
 2 GQ 3

Db

Search completed: August 23, 2004, 10:53:59  
 Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:48:20 ; Search time 112 Seconds  
(without alignments)  
25.354 Million cell updates/sec

25.354 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQVMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: SP archaea:\*
  - 2: SP bacteria:\*
  - 3: SP fungi:\*
  - 4: SP human:\*
  - 5: SP\_invertebrate:\*
  - 6: SP\_mammal:\*
  - 7: SP\_mhc:\*
  - 8: SP\_organelle:\*
  - 9: SP\_phage:\*
  - 10: SP\_plant:\*
  - 11: SP\_rodent:\*
  - 12: SP\_virus:\*
  - 13: SP\_vertebrate:\*
  - 14: SP\_unclassified:\*
  - 15: SP\_virus:\*
  - 16: SP\_bacteriaph:\*
  - 17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	40.4	9	4 Q96P97	Q96P97 homo sapien
2	19	40.4	9	10 Q81P75	Q81P75 zea mays (m
3	18	38.3	8	12 Q80H91	Q80H91 newcastle d
4	18	38.3	9	4 Q81UJ5	Q81UJ5 homo sapien
5	17	36.2	8	4 Q9P285	Q9P285 homo sapien
6	17	36.2	8	11 Q9QV15	Q9QV15 ratcus sp.
7	16	34.0	8	13 Q9G493	Q9G493 eopsaltria
8	16	34.0	9	10 Q42452	Q42452 tritlicum ae
9	15	31.9	9	1 Q50832	Q50832 methanococ
10	15	31.9	9	2 P72149	P72149 pseudomonas
11	14	29.8	7	2 P83530	P83530 lactobacill
12	14	29.8	8	4 Q86510	Q86510 homo sapien
13	14	29.8	8	5 Q9N6M5	Q9N6M5 toxoplasma
14	14	29.8	8	10 Q42507	Q42507 tritlicum ae
15	14	29.8	9	12 Q88953	Q88953 vaccinia vi
16	13	27.7	8	2 Q51594	Q51594 escherichia

17	13	27.7	8	5 Q9UB13	Q9UB13 albinaria h
18	13	27.7	8	5 Q94695	Q94695 physarum po
19	13	27.7	9	2 Q51765	Q51765 pseudomonas
20	13	27.7	9	6 Q8MJ78	Q8MJ78 eulemur ful
21	13	27.7	9	6 Q8MJ78	Q8MJ78 eulemur ful
22	12	25.5	8	4 Q9U50	Q9U50 homo sapien
23	12	25.5	8	4 Q9H4D3	Q9H4D3 homo sapien
24	12	25.5	8	5 Q9TWH6	Q9TWH6 perinearis
25	12	25.5	8	6 Q8WNS1	Q8WNS1 bos taurus
26	12	25.5	8	10 Q40659	Q40659 oryza sativ
27	12	25.5	9	2 Q931E4	Q931E4 heliobacill
28	12	25.5	9	2 Q937F8	Q937F8 escherichia
29	12	25.5	9	2 Q9R735	Q9R735 streptomyce
30	12	25.5	9	2 Q937H9	Q937H9 enterobacte
31	12	25.5	9	2 Q7X4R7	Q7X4R7 neisseria m
32	12	25.5	9	11 Q9QZ88	Q9QZ88 mus musculu
33	12	25.5	9	13 Q8UJ12	Q8UJ12 carassius a
34	12	25.5	9	13 Q8UJ10	Q8UJ10 danio frank
35	12	25.5	9	13 Q8UJ16	Q8UJ16 danio albol
36	12	25.5	9	13 Q15897	Q15897 homo sapien
37	11	23.4	7	4 Q9R3X0	Q9R3X0 planktothri
38	11	23.4	8	2 Q9ZE29	Q9ZE29 buchiera ap
39	11	23.4	8	2 Q45889	Q45889 clostridium
40	11	23.4	8	2 Q81V87	Q81V87 homo sapien
41	11	23.4	8	4 Q94623	Q94623 manduca sex
42	11	23.4	8	5 Q9ET18	Q9ET18 mus spretus
43	11	23.4	8	11 Q9ET17	Q9ET17 mus caroli
44	11	23.4	8	11 Q9ET16	Q9ET16 mesocricetu
45	11	23.4	8	11 Q9ET16	Q9ET16 mesocricetu

ALIGNMENTS

RESULT 1

ID Q96P97 PRELIMINARY; PRT; 9 AA.

AC Q96P97; (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE Reptin52 protein (Fragment).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.; "Characterization of TPA-responsive genes in U937 cells using ordered RT differential display PCR."; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF401216; AAL02172.1; --.

FT NON TER 1 1

FT SEQUENCE 9 AA; 981 MW; SCDDAA681AB1873 CRC64;

Query Match 40.4%; Score 19; DB 4; Length 9;  
Best local Similarity 60.0%; Pred. No. 1e+06;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQVMD 7

DB 3 GETMD 7

RESULT 2

ID Q81P75 PRELIMINARY; PRT; 9 AA.

AC Q81P75; (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)

DE Beta-expansin-like protein (Fragment).

OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 RX NCB1\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. C123;  
 RA Chung A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
 RT "SNP frequency, haplotype structure and linkage disequilibrium in  
 elite maize inbred lines."  
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY094310; AAM21836.1; --  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 977 MW; 5C05B2D2CB1AAA3 CRC64;

Query Match 40.4%; Score 19; DB 10; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 1e+06;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMD 7  
 :|:|:  
 Db 2 KDEVDV 8

RESULT 3  
 Q80H91 PRELIMINARY; PRT; 8 AA.  
 AC Q80H91;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DE HN/HNO (Fragment).  
 GN HN/HNO.  
 OS Newcastle disease virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirinae;  
 OC NCB1\_TaxID=11176;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=94175786; PubMed=8129624;  
 RA Collins M.S., Strong I., Alexander D.J.;  
 RT "Evaluation of the molecular basis of pathogenicity of the variant  
 Newcastle disease viruses termed 'pigeon FMV-1 viruses'."  
 RL Arch. Virol. 134:403-411(1994).  
 DR EMBL; S69419; AAP19628.1; --  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 929 MW; 33D4087AA337205B CRC64;

Query Match 38.3%; Score 18; DB 12; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGOV 5  
 :|:|:  
 Db 4 KDGGRV 8

RESULT 4  
 Q81U05 PRELIMINARY; PRT; 9 AA.  
 AC Q81U05;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Transforming, acidic coiled-coil containing protein 1 variant TACCl-B  
 (Fragment).  
 GN TACCl.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RX NCB1\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISU8-Stomach cancer;  
 RA Line A., Slucka Z., Stengrevics A., Li G., Rees R.C.;  
 RT "Altered Splicing Pattern of TACCl mRNA in Gastric Cancer."  
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY072873; AAL62460.2; --  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 980 MW; 790BD1B5B87AAB1B CRC64;

Query Match 38.3%; Score 18; DB 4; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGOVM 6  
 :|:|:  
 Db 3 EDGTV 8

RESULT 5  
 Q9P285 PRELIMINARY; PRT; 8 AA.  
 AC Q9P285;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE Clotting factor VIII (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shibata M., Shima M., Morichika S., Yoshioka A.;  
 RT "Human clotting factor VIII gene, junction regions of the deletion of  
 exon 4 through 7."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB040872; BAA94312.1; --  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 36.2%; Score 17; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDG 3  
 :|:  
 Db 4 EDG 6

RESULT 6  
 Q9QV15 PRELIMINARY; PRT; 8 AA.  
 AC Q9QV15;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE 18 kDa cell growth factor (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RX NCB1\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=92028975; PubMed=1656977;  
 RA Malner P.G.;  
 RT "Simian sarcoma virus transformation of normal rat kidney fibroblasts  
 is associated with markedly increased basic fibroblast growth factor  
 expression."  
 RL Biochem. Biophys. Res. Commun. 180:423-430(1992).  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

SQ SEQUENCE 8 AA; 807 MW; B0787AAB07673AFA CRC64;

Query Match  
Best Local Similarity 36.2%; Score 17; DB 11; Length 8;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDG 3  
|||  
5 EDG 7

RESULT 7

ID 090493 PRELIMINARY; PRT; 8 AA.

AC 090493;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE Myoglobin (Fragment).  
OS Eopsaltria australis (eastern yellow robin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Petroicidae; Eopsaltria.  
OX NCBI\_TaxID=43318;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EL5;  
RX MEDLINE=98208049; PubMed=9548272;  
RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;  
RT "Myoglobin interon variation in the Gouldian Finch Erythrura gouldiae  
assessed by temperature gradient gel electrophoresis.";  
RL Electrophoresis 19:142-151(1998).  
DR EMBL; U40495; AAC60362.1; -.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 921 MW; C6CAB2DAF5B046DE CRC64;

Query Match  
Best Local Similarity 34.0%; Score 16; DB 13; Length 8;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 QVMDVD 9  
|:|  
2 QISXVD 7

RESULT 8

ID 042452 PRELIMINARY; PRT; 9 AA.

AC 042452;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Heat shock protein (Fragment).  
GN HSP266T1 OR HSP266G2.  
OS Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OX Triticaceae; Triticum.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV MUSTANG;  
RA Joshi C.P., Kluve N., Nguyen H.T.;  
RT Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; L41504; AAA64972.1; -.  
DR GO; GO:0003773; F:heat shock protein activity; IEA.  
KW Heat shock.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 1084 MW; 4658C322CA042C3 CRC64;

Query Match  
Best Local Similarity 34.0%; Score 16; DB 10; Length 9;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 QVMDV 8  
|:|  
2 KVIDV 6

RESULT 9

ID 050832 PRELIMINARY; PRT; 9 AA.

AC 050832;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)  
DE Intergenic AT-rich DNA sequence (Fragment).  
OS Methanococcus voltae.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanococcaceae; Methanococcus.  
OX NCBI\_TaxID=2188;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85230552; PubMed=406907;  
RA Bollschweiler C., Kuehn R., Klein A.;  
RT "Non-repetitive AT-rich sequences are found in intergenic regions of  
Methanococcus voltae DNA.";  
RL EMBL; X02518; CAA26355.1; -.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1087 MW; 99ED005DC404405A CRC64;

Query Match  
Best Local Similarity 31.9%; Score 15; DB 1; Length 9;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 MDVD 9  
|:|  
1 MDIN 4

RESULT 10

ID P72149 PRELIMINARY; PRT; 9 AA.

AC P72149;  
DT 01-FEB-1997 (TREMBlrel. 02, Created)  
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Putative glucokinase (Fragment).  
GN GK.

OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PA01;  
RX MEDLINE=96427344; PubMed=8830708;  
RA Sage A.E., Proctor W.D., Phibbs P.V.Jr.;  
RT "A two-component response regulator, gltR, is required for glucose  
transport activity in Pseudomonas aeruginosa PA01.";  
RL J. Bacteriol. 178:6064-6066(1996).  
DR EMBL; U50932; AAC44474.1; -.  
DR GO; GO:0016501; F:kinase activity; IEA.  
KW Kinase.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 944 MW; C3071DDAA72DC66 CRC64;

Query Match  
Best Local Similarity 31.9%; Score 15; DB 2; Length 9;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 QVMDVD 9  
|:|  
3 QALDAE 8

```

RESULT 11
ID P83530 PRELIMINARY; PRT; 7 AA.
AC P83530;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Georg A.;
RT "High pressure effects step-wise altered protein expression in
  Lactobacillus sanfranciscensis."
RC Procomics 2:765-774(2002).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
  PROTEIN IS: 15 KDA.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 2; Length 7;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 MDVD 9
  :||:
Db 3 LDVE 6

RESULT 12
ID Q86SL0 PRELIMINARY; PRT; 8 AA.
AC Q86SL0;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Flavocytochrome b-558 alpha polypeptide (Fragment).
OS CYBA.
GN Homo sapiens (Human).
OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22615572; PubMed=12729892;
RA Moreno M.U., San Jose G., Orde J., Paramo J.A., Belouqui O., Diez J.,
  Zalba G.;
RT "Preliminary characterisation of the promoter of the human p22phox
  gene: identification of a new polymorphism associated with
  hypertension."
RT FBS Lett. 542:27-31(2003).
RL EMBL; AY128666; AAM96953.1; -.
DR EMBL; AY128666; AAM96953.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 965 MW; FFDG37B1046D876 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 4; Length 8;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GOV 5
  :||:
Db 2 GQI 4

```

RESULT 13

```

O9N6M5
ID O9N6M5 PRELIMINARY; PRT; 8 AA.
AC O9N6M5;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE Dihydrofolate reductase thymidylate synthase (Fragment).
GN FOL1.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH, COUGAR TC751G34, SEA OTTER TC928G1, and BEVERLEY;
RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and
  Housekeeping Genes."
RT J. Parasitol. 0:0-0(2000).
RL EMBL; AF249695; AAF79153.1; -.
DR EMBL; AF249692; AAF79150.1; -.
DR EMBL; AF249693; AAF79151.1; -.
DR EMBL; AF249694; AAF79152.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1035 MW; 33CAAA05B133044 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 5; Length 8;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVMDVD 9
  :||:
Db 1 RIKEID 6

```

```

RESULT 14
ID Q42507 PRELIMINARY; PRT; 8 AA.
AC Q42507;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Heat shock protein (Fragment).
GN HSP70C OR HSP70A OR HSP70B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV MUSTANG.
RX MEDLINE=9619275; PubMed=8605312;
RA Joshi C.P., Kumar S., Nguyen H.T.;
RT "Application of modified differential display technique for cloning
  and sequencing of the 3' region from three putative members of wheat
  HSP70 gene family."
RL Plant Mol. Biol. 30:641-646(1996).
DR EMBL; L41507; AAB02333.1; -.
DR EMBL; L41505; AAB02331.1; -.
DR EMBL; L41506; AAB02332.1; -.
DR GO; GO:0003773; F:heat shock protein activity; IEA.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 886 MW; 71B2CB1B10532768 CRC64;

Query Match
Best Local Similarity 29.8%; Score 14; DB 10; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVMDVD 9
  :||:

```

Db 3 KIEEVD 8

RESULT 15

Q88953 PRELIMINARY; PRT; 9 AA.  
 AC Q88953;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)  
 DE Serpins (Fragment).  
 GN B13R/SPI-2.  
 OS Vaccinia virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=10245;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9513144; PubMed=7831769;  
 RA Kettle S., Blake N.W., Law K.M., Smith G.L.;  
 RT "Vaccinia virus serpins B13R (SPI-2) and B22R (SPI-1) encode M(r) 38.5  
 RT and 40K, intracellular polypeptides that do not affect virus virulence  
 RT in a murine intranasal model.";  
 RL Virology 206:136-147(1995).  
 DR EMBL; S75133; AAC60736.1; -.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1081 MW; 9E84D05B0409C05A CRC64;

Query Match 29.8%; Score 14; DB 12; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MDV 8  
 ||:  
 Db 1 MDI 3

Search completed: August 23, 2004, 10:55:59  
 Job time : 116 secs

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Page Blank (uspto)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2004, 10:32:29 ; Search time 38 Seconds

(without alignments)  
22.782 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQVMDVD 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*\*

1: p1r1:\*\*  
2: p1r2:\*\*  
3: p1r3:\*\*  
4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match Length DB	ID	Description
1	47	100.0	426 2	Ig epsilon-chain -
2	47	100.0	428 1	Ig epsilon-chain -
3	38	80.9	118 2	50S ribosomal prot
4	36	76.6	480 2	hypothetical prote
5	36	76.6	655 2	threonyl-tRNA synt
6	35	74.5	198 2	probable transcrip
7	35	74.5	265 2	hypothetical prote
8	35	74.5	846 2	primosomal protein
9	35	74.5	1275 2	hypothetical prote
10	35	74.5	1275 2	hypothetical prote
11	34	72.3	203 2	probable transcrip
12	34	72.3	210 2	hypothetical prote
13	34	72.3	264 2	hypothetical prote
14	34	72.3	266 2	hypothetical prote
15	34	72.3	561 2	DNA ligase [import
16	34	72.3	677 2	sensory transduct
17	34	72.3	841 2	preprotein transi
18	34	72.3	1379 2	YTA7 protein - yea
19	33	70.2	189 2	dnaU protein - syn
20	33	70.2	287 2	dnaU protein - syn
21	33	70.2	314 2	geranylgeranyl dip
22	33	70.2	347 2	beta-alanine-Pyruv
23	33	70.2	448 2	probable ABC trans
24	33	70.2	503 2	probable kinase/ph
25	33	70.2	634 2	probable protein k
26	33	70.2	725 2	hypothetical prote
27	33	70.2	960 2	hypothetical prote
28	33	70.2	1155 2	probable protein k
29	33	70.2	1491 2	hypothetical prote

30	32	68.1	95	2	I40330	Cpn10 protein (Gro
31	32	68.1	98	2	A37397	hypothetical prote
32	32	68.1	121	2	H64350	hypothetical prote
33	32	68.1	173	2	T24207	hypothetical prote
34	32	68.1	180	2	S52640	hypothetical prote
35	32	68.1	226	2	A97340	ABC-type transport
36	32	68.1	240	2	S61872	hypothetical prote
37	32	68.1	273	2	B23971	monophenol monooxy
38	32	68.1	314	2	AB3610	multidrug resistan
39	32	68.1	379	2	D70786	probable gcvT prot
40	32	68.1	398	2	B84888	probable methionin
41	32	68.1	408	2	C86799	hypothetical prote
42	32	68.1	421	2	T00955	hypothetical prote
43	32	68.1	443	2	D86183	hypothetical prote
44	32	68.1	501	1	P1WLEP	I1 protein - Europ
45	32	68.1	508	1	P1WLE	I1 protein - human

#### ALIGNMENTS

##### RESULT 1

I36948

Ig epsilon-chain - chimpanzee (fragment)

C/Species: Pan troglodytes (chimpanzee)

C/Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000

C/Accession: I36948

R/Sakoyama, Y.; Hong, K. Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987

A/Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan

A/Reference number: I36948; NCBI:87147196; PMID:3103123

A/Accession: I36948

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-426 <RES>

A/Cross-references: GB:M15398; NID:9176797; PIDN:AAA35416.1; PID:9176798

C/Genetics: A.Intlons: 103/1; 209/1; 317/1

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F/336-405/Domain: immunoglobulin homology <IMM>

Query Match	Best Local Similarity	Score 47; DB 2; Length 426;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 EDGQVMDVD 9	
Db	149 EDGQVMDVD 157	

##### RESULT 2

EHNU

Ig epsilon chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1981 #sequence\_revision 13-Jun-1983 #text\_change 16-Jul-1999

C/Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C461

R/Flanagan, J.G.; Rabbits, T.H. EMBO J. 1, 655-660, 1982

A/Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene,

A/Reference number: A22771; NCBI:84236029; PMID:6234164

A/Accession: A22771

A/Molecule type: DNA

A/Residues: 1-428 <FLA>

A/Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:9185035

R/Ueda, S.; Nakai, S.; Nishida, Y.; Hisejima, H.; Honjo, T. EMBO J. 1, 1539-1544, 1982

A/Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudoge

A/Reference number: A23195; NCBI:84207910; PMID:6327276

A/Accession: A23195

A/Molecule type: DNA

A/Residues: 2-428 <UED>

A/Cross-references: GB:J00222; NID:9184755

R/Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992  
 A>Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing  
 A:Reference number: P11214; MUID:92308839; PMID:1613458  
 A:Accession: P11214  
 A:Molecule type: DNA  
 A:Residues: 320-428 <ZHA>  
 A:Cross-references: EMBL:X63693; GB:S38668; NID:93232987  
 R:Geno, M.; Kurokawa, T.; Ono, Y.; Onde, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugii  
 Nucleic Acids Res. 11, 719-726, 1983  
 A>Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha  
 A:Reference number: A93491; MUID:83168897; PMID:6300763  
 A:Accession: A93491  
 A:Molecule type: mRNA  
 A:Residues: 1-428 <SEN>  
 A:Cross-references: GB:L00022; GB:U00227; GB:V00555; NID:9185035  
 R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.  
 Cell 29, 691-699, 1982  
 A>Title: Duplication and deletion in the human immunoglobulin epsilon genes.  
 A:Reference number: A90824; MUID:83001945; PMID:6288268  
 A:Accession: A90824  
 A:Molecule type: DNA  
 A:Residues: 1-358, 'L', 360-428 <MAX>  
 A:Cross-references: GB:J00222; NID:9184755  
 A:Note: this sequence difference may be due to polymorphism  
 R:Benich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.  
 in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3  
 A:Reference number: A94418  
 A:Accession: A94418  
 A:Molecule type: protein  
 A:Residues: 'GAWTL', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12  
 A:Experimental source: myeloma protein Nd  
 R:Kreiken, J.H.; Molgaard, H.V.; Houghton, M.; Derjshvire, R.B.; Vlnay, J.; Bell, L.O.; G  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982  
 A>Title: Cloning and sequence determination of the gene for the human immunoglobulin eps  
 A:Reference number: A93933; MUID:83065234; PMID:6815656  
 A:Accession: B93933  
 A:Molecule type: mRNA  
 A:Residues: 1-40; 68-114; 427-428 <KEN>  
 A:Cross-references: GB:U00022; NID:9185035  
 R:Keyama, S.  
 FEBS Lett. 224, 306-310, 1987  
 A>Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment  
 A:Reference number: S02438; MUID:88083554; PMID:3121387  
 A:Accession: S02438  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 98-352 <1KE>  
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.  
 J. Biol. Chem. 269, 456-462, 1994  
 A>Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces  
 A:Reference number: A53116; MUID:94103254; PMID:8276835  
 A:Accession: A53116  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 320-428 <ZHE>  
 A:Experimental source: myeloma U266-derived cell line AF-10  
 A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)  
 R:Helman, L.  
 Eur. J. Immunol. 23, 159-167, 1993  
 A>Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of  
 A:Reference number: A46536; MUID:93122085; PMID:8419166  
 A:Accession: C46536  
 A:Molecule type: mRNA  
 A:Status: preliminary; not compared with conceptual translation  
 A:Residues: 382-426 <HEL>  
 A:Cross-references: GB:S55273; NID:9263166; PIDN:AAB24857.1; PID:9263167  
 A:Experimental source: B cell myeloma U-266  
 A:Note: sequence extracted from NCBI backbone (NCBIP:125297)  
 A:Accession: D46536  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 382-391 <HE2>  
 A:Cross-references: GB:S55276; NID:9263168; PIDN:AAB24858.1; PID:9263169

A:Experimental source: B cell myeloma U-266  
 A:Note: sequence extracted from NCBI backbone (NCBIP:125299)  
 A:Accession: A46536  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 401-428 <HE3>  
 A:Cross-references: GB:S53497; NID:9263162; PIDN:AAB24855.1; PID:9263163  
 A:Experimental source: B cell myeloma U-266  
 A:Note: sequence extracted from NCBI backbone (NCBIP:123483)  
 C:Genetics:  
 A:Gene: GDB:IGHB  
 A:Cross-references: GDB:119335; OMIM:147180  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 1/1; 104/1; 211/1; 319/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat  
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu  
 F:122-87/Domain: immunoglobulin homology <IM1>  
 F:128-195/Domain: immunoglobulin homology <IM2>  
 F:232-301/Domain: immunoglobulin homology <IM3>  
 F:338-407/Domain: immunoglobulin homology <IM4>  
 F:114/Disulfide bonds: interchain (to light chain) #status predicted  
 F:15-105,29-85,135-193,239-259,345-405/Disulfide bonds: #status predicted  
 F:21,49,99,146,252,275/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 100.0%; Score 47; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 0.26; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;  
 QY 1 EDGQVMDVD 9  
 |||||  
 Db 151 EDGQVMDVD 159

RESULT 3  
 G84322  
 50S ribosomal protein L24P [imported] - Halobacterium sp. NRC-1  
 C:Species: Halobacterium sp. NRC-1  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #extl\_change 16-Feb-2001  
 C:Accession: G84322  
 R:Ng, W.V.; Kennedy, S.P.; Mahaitas, G.G.; Bergquist, B.; Par, M.; Shukla, H.D.; Lasky, S.  
 ; Leithauser, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor  
 Jung, K.H.; Alam, M.; Freltas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
 A>Title: Genome sequence of Halobacterium species NRC-1  
 A:Reference number: A84160; MUID:20504483; PMID:11016950  
 A:Accession: G84322  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-118 <STO>  
 A:Cross-references: GB:AE004437; NID:910581170; PIDN:AA319947.1; GSPDB:GN00138  
 C:Genetics:  
 A:Gene: rpl24P  
 C:Superfamily: rat ribosomal protein L26

Query Match 80.9%; Score 38; DB 2; Length 118;  
 Best Local Similarity 77.8%; Pred. No. 3.3; Indels 1; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0;  
 QY 1 EDGQVMDVD 9  
 |||||  
 Db 59 EDGEVTDVD 67

RESULT 4  
 T46047  
 Hypothetical protein T16K5.160 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C:Accession: T46047

R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000  
A;Reference number: Z23015  
A;Accession: T746047  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-480 <RIB>  
A;Cross-references: EMBL:AL132965  
A;Experimental source: cultivar Columbia; BAC clone T16K5  
C;Genetics:  
A;Map position: 3  
A;Intons: 420/2; 451/3  
A;Note: T16K5.160

Query Match  
Best Local Similarity 76.6%; Score 36; DB 2; Length 480;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGVMDVD 9  
DB 20 DQGVLDLD 27

RESULT 5  
G87306  
thrcyyl-*tRNA synthetase* [imported] - *Caulobacter crescentus*  
C;Species: *Caulobacter crescentus*  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C;Accession: G87306  
R;Nierman, W.C.; Feildblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of *Caulobacter crescentus*.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: G87306  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-655 <STO>  
A;Cross-references: GB:AE005673; NID:913421637; PIDN:AAK22451.1; GSPDB:GN00148  
C;Genetics:  
A;Gene: CC0464  
C;Superfamily: threonine-*tRNA* ligase

Query Match  
Best Local Similarity 76.6%; Score 36; DB 2; Length 655;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQGVMDVD 9  
DB 41 DQGVLDLD 48

RESULT 6  
E81391  
probable transcription regulator Cj0466 [imported] - *Campylobacter jejuni* (strain NCTC 1  
C;Species: *Campylobacter jejuni*  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C;Accession: E81391  
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Varley, A.; Whitehead, S.; Barral  
Nature 403, 665-668, 2000  
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp  
A;Reference number: A81250; MUID:20150912; PMID:10688204  
A;Accession: E81391  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-198 <PAR>  
A;Cross-references: GB:AL139075; GB:AL111168; NID:96967817; PIDN:CBW75104.1; PID:9696793  
C;Experimental source: serotype O2, strain NCTC 11168  
C;Genetics:  
A;Gene: Cj0466

Query Match  
Best Local Similarity 74.5%; Score 35; DB 2; Length 198;  
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDQGVMDVD 9  
DB 83 EDGEILRID 91

RESULT 7  
E69160  
hypothetical protein MTH462 - *Methanobacterium thermoautotrophicum* (strain Delta H)  
C;Species: *Methanobacterium thermoautotrophicum*  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C;Accession: E69160  
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F  
ki, S.; Church, G.M.; Daniels, C.U.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functi  
A;Reference number: A69000; MUID:98037514; PMID:9371463  
A;Accession: E69160  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-265 <MTH>  
A;Cross-references: GB:AE000830; GB:AE000665; NID:92621523; PIDN:AMB84968.1; PID:92621530  
C;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH462

Query Match  
Best Local Similarity 74.5%; Score 35; DB 2; Length 265;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDQGVMDVD 9  
DB 155 EDGEIVDE 163

RESULT 8  
A12336  
ribosomal protein N' [imported] - *Nostoc* sp. (strain PCC 7120)  
C;Species: *Nostoc* sp. strain PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C;Accession: A12336  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Matsumoto, A.; Iriyuchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anat*  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: A12336  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-846 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BBW75947.1; PID:91713383; GSPDB:GN00179  
C;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all4248

Query Match  
Best Local Similarity 74.5%; Score 35; DB 2; Length 846;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQGVMDVD 9  
DB 280 EDQGVLDLD 288

RESULT 9  
T49362  
hypothetical protein Bld1.160 [imported] - *Neurospora crassa*  
C;Species: *Neurospora crassa*

C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C/Accession: T49362  
R/Schulte, U.; Aign, V.; Hohsels, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura, R.  
Submitted to the Protein Sequence Database, May 2000  
A/Reference number: Z25022  
A/Accession: T49362  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1275 <SCH>  
A/Cross-references: EMBL:AL355927, GSPDB:GN00116, NCSP:BLD1.160  
A/Experimental source: BAC clone BLD1, strain OR74A  
C/Genetics:  
A/Gene: NCSP:BLD1.160  
A/Map position: 6  
A/Introns: 24/3

Query Match 74.5%; Score 35; DB 2; Length 1275;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
DB 1116 EDGQWMDVD 1124

RESULT 10  
T16580  
hypothetical protein K07E12.1 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C/Accession: T16580  
R/Fulton, L.  
Submitted to the EMBL Data Library, May 1994  
A/Description: The sequence of C. elegans cosmid K07E12.  
A/Reference number: Z18540  
A/Accession: T16580  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-13055 <FLU>  
A/Cross-references: EMBL:U00054; NID:G485140; PID:G485141; PIDN:AAA50715.1; CESP:K07E12.  
A/Experimental source: strain Bristol N2  
C/Genetics:  
A/Gene: CESP:K07E12.1  
A/Introns: 46/3; 85/2; 201/1; 278/2; 470/2; 817/1; 927/1; 960/3; 1265/1; 1322/1; 1478/3;  
; 6014/3; 6159/3; 6665/2; 7266/3; 7895/3; 8669/3; 8726/3; 9803/3; 10937/3; 12234/2; 1229

Query Match 74.5%; Score 35; DB 2; Length 13055;  
Best Local Similarity 55.6%; Pred. No. 2.6e+03;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
DB 11710 EDGQWMDVD 11718

RESULT 11  
C95882  
probable transcription regulator protein [imported] - Sinorhizobium meliloti (strain 102)  
C/Species: Sinorhizobium meliloti  
C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C/Accession: C95882  
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernat  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo  
A/Reference number: A95842; MUID:21396508; PMID:11481431  
A/Accession: C95882  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-203 <KUR>  
A/Cross-references: GB:AL591985; PIDN:CAC48723.1; PID:G15140196; GSPDB:GN00167  
A/Experimental source: strain 1021, megaplasmid pSymB  
R/Galbert, F.; Finan, T.M.; Jorg, S.R.; Fulter, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LeJaure,  
heban, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C  
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A/Reference number: A96039; MUID:21368234; PMID:11474104  
C/Genetics:  
A/Contents: annotation  
A/Gene: Smb20337  
A/Genome: plasmid

Query Match 72.3%; Score 34; DB 2; Length 203;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQWMDVD 9  
DB 148 DGEVIDID 155

RESULT 12  
D96531  
hypothetical protein F13F21.9 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C/Accession: D96531  
R/Theologis, A.; Ecker, J.R.; Palm, C.D.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Comu, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:2106719; PMID:11130712  
A/Accession: D96531  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-210 <STO>  
A/Cross-references: GB:AE005173; NID:G5430754; PIDN:AAA43154.1; GSPDB:GN00141  
C/Genetics:  
A/Gene: F13F21.9  
A/Map position: 1

Query Match 72.3%; Score 34; DB 2; Length 210;  
Best Local Similarity 55.8%; Pred. No. 38;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQWMDVD 9  
DB 136 DGEVIDID 144

RESULT 13  
B90535  
hypothetical protein MYPU 1860 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
C/Species: Mycoplasma pulmonis  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
C/Accession: B90535  
R/Chamand, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
A/Reference number: A95612; MUID:21267165; PMID:11353084  
A/Accession: B90535  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-264 <KUR>  
A/Cross-references: GB:AL445566; PID:G14089599; PIDN:CAC13359.1; GSPDB:GN00153  
A/Experimental source: strain UAB CTIP  
C/Genetics:  
A/Gene: MYPU\_1860

A:Genetic code: SGC3

Query Match 72.3%; Score 34; DB 2; Length 264;  
 Best Local Similarity 44.4%; Pred. No. 49;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
 :||:|:|:  
 Db 96 QDGNLIDID 104

## RESULT 14

D69272

hypochemical protein AF0180 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

C/Accession: D69272

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirtress, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaime, B.P.; Sykes, S.

Smith, H.O.; Moese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A/Reference number: A69250; MUID:98049343; PMID:9389475

A/Accession: D69272

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1286 &lt;KE&gt;

A/Cross-references: GB:AE001093; GB:AE000782; NID:G2689416; PIDN:AB91050.1; PID:G265046

## Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 286;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMD 7  
 |||:|:  
 Db 7 EDGQVMD 13

## RESULT 15

G84244

DNA ligase [imported] - Halobacterium sp. NRC-1

C/Species: Halobacterium sp. NRC-1

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C/Accession: G84244

R/Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabcic

ung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A/Title: Genome sequence of Halobacterium species NRC-1.

A/Reference number: A84160; MUID:20504483; PMID:11016950

A/Accession: G84244

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1561 &lt;STO&gt;

A/Cross-references: GB:AE004437; NID:G10580445; PIDN:AA919323.1; GSPDB:GN00138

C/Genetics:

A:Gene: lig

C/Superfamily: DNA ligase

## Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 561;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9  
 |||:|:|:  
 Db 497 EDGQVMDIE 505

Search completed: August 23, 2004, 10:40:37  
 Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:40:45 ; Search time 121 Seconds

(without alignments)  
21.016 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQVMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	3 AAB25907	Aab25907 IGE C-eps
2	47	100.0	9	3 AAB20867	Aab20867 Immunoglob
3	47	100.0	9	4 AAB51023	Aab51023 IGE pepit
4	47	100.0	9	4 AAUI6632	Aau16632 Peptide P
5	47	100.0	9	5 ABUT00217	Abj00217 Human IGE
6	47	100.0	9	7 ADE10893	Ade10893 Chimeric
7	31	66.0	9	6 AAB35091	Aae35091 Human imm
8	30	63.8	7	3 AAB25923	Aab25923 PI mimoto
9	30	63.8	7	4 AAUI6648	Aau16648 Peptide P
10	30	63.8	7	5 ABUT00227	Abj00227 Human IGE
11	30	63.8	9	6 AAB35076	Aae35076 Human imm
12	28	59.6	7	5 AAE14481	Aae14481 Ophiophor
13	28	59.6	9	5 ABJ12821	Abj12821 Human 125
14	26	55.3	9	6 AAB35101	Aae35101 Human imm
15	25	53.2	9	5 ABG67564	Abg67564 Human ADP
16	25	53.2	9	6 ADA23680	Aad23680 Human imm
17	25	53.2	9	6 AAB35082	Aae35082 Human ADP
18	23	48.9	8	2 AAR6589	Aar6589 Alzheim
19	23	48.9	8	6 AAB63684	Aab63684 Human bre
20	23	48.9	9	2 AAR29631	Aar29631 Adhesion
21	23	48.9	9	2 AAR28886	Aar28886 Cell adhe
22	23	48.9	9	2 AAR30433	Aar30433 Cell adhe
23	23	48.9	9	7 ADC70686	Adc70686 HLA motif
24	23	48.9	9	7 ADC70771	Adc70771 HLA motif
25	22	46.8	6	2 AAY42592	Aay42592 Human IGE

26	22	46.8	7	3 AAY61779	Aay61779 Cadherin-
27	22	46.8	7	5 AAUB1643	AauB1643 Enterokin
28	22	46.8	7	5 ABUT79925	Abu79925 Enterokin
29	22	46.8	8	2 ADC81362	Adc81362 Bovin THF
30	22	46.8	8	3 AAY61785	Aay61785 Cadherin-
31	22	46.8	9	2 AAY00372	Aay00372 Fragment
32	22	46.8	9	3 AAY61788	Aay61788 Immunogen
33	22	46.8	9	2 AAY48066	Aay48066 Cadherin-
34	22	46.8	9	5 ABJ13116	Abj13116 Human 125
35	22	46.8	9	5 ABJ13305	Abj13305 Human 125
36	22	46.8	9	6 ABUT0192	Abu0192 MHC bindi
37	22	46.8	9	7 AAD90448	Add90448 Novel hum
38	21	44.7	7	2 AAW63724	Aaw63724 C. histol
39	21	44.7	8	2 ADC81368	Adc81368 Bovin THF
40	21	44.7	8	5 AAE25317	Aae25317 Human UST
41	21	44.7	9	2 AAW15176	Aaw15176 Chlamydia
42	21	44.7	9	2 AAW40838	Aaw40838 Cytotoxic
43	21	44.7	9	2 AAY30292	Aay30292 Angiopoie
44	21	44.7	9	3 AAB03468	Aab03468 Human tyr
45	21	44.7	9	4 AAB49428	Aab49428 Peptide #

## ALIGNMENTS

RESULT 1  
AAB25907  
ID AAB25907 standard; peptide; 9 AA.  
AC AAB25907;  
DT 05-JAN-2001 (first entry)  
DE IGE C-epsilon-2 domain surface exposed epitope peptide P1 SEQ ID NO:1.  
XX  
XX  
KW Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;  
KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.  
OS Homo sapiens.  
XX  
XX  
PN W0200050460-A1.  
XX  
XX  
PD 31-AUG-2000.  
XX  
XX  
PF 22-FEB-2000; 2000MC-EP001455.  
XX  
XX  
PR 25-FEB-1999; 99GB-00004405.  
PR 29-MAR-1999; 99GB-00007151.  
PR 07-MAY-1999; 99GB-00010537.  
PR 07-MAY-1999; 99GB-00010538.  
PR 07-AUG-1999; 99GB-00018594.  
PR 07-SEP-1999; 99GB-00018603.  
PR 07-SEP-1999; 99GB-00021046.  
PR 07-SEP-1999; 99GB-00021047.  
PR 29-OCT-1999; 99GB-00025619.  
PR 23-NOV-1999; 99GB-00027698.  
XX  
XX  
PA (SMRK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Baesolac;  
XX  
XX  
DR WPI; 2000-572073/53.  
XX  
XX  
PT Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.  
XX  
XX  
PS Claim 2; Page 5; 129pp; English.  
XX

CC The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (1a) capable of being recognised by (IV); (6) an immunogen  
CC (IIa) comprising (1a); and (7) producing (III) by producing (II). (I) can  
CC have anti-allergic and immunosuppressive activities, and can be used as a  
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
CC in medicine and in the manufacture of medicaments for treating and  
CC preventing allergies. (IV) is useful for identifying mimotopes of PI, in  
CC medicine and also in manufacturing medicaments for treating allergies.  
CC (I) is useful in diagnostics and in the affinity purification of  
CC circulating anti-IgE antibodies from blood. (I), (III) and PC are useful  
CC for treating a patient susceptible to or suffering from allergies. (IV)  
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention  
CC XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 47; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVD 9  
DB 1 EDGQVMDVD 9  
RESULT 2  
AAB20867  
ID AAB20867 standard; peptide; 9 AA.  
XX AAB20867;  
XX DT 03-JAN-2001 (first entry)  
XX DE Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.  
XX DE Immunoglobulin E; IGE; immunogenic; immunogen; Protein D; carrier;  
XX KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;  
XX KW malaria; cytostatic; anti-allergic; nocrotropic; neuroprotective;  
XX KW protozoacide; Alzheimer's disease; allergy.  
XX OS Homo sapiens.  
XX PN WO200050077-A1.  
XX PD 31-AUG-2000.  
XX PF 22-FEB-2000; 2000WO-EP001457.  
XX PR 25-FEB-1999; 99GB-000004405.  
XX PR 25-FEB-1999; 99GB-000004408.  
XX PR 25-FEB-1999; 99GB-00004412.  
XX PR 13-AUG-1999; 99GB-00019260.  
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PI Coste M, Lobet Y, Van-Mechelen MP, Verriest C;  
XX DR WPI; 2000-572040/53.  
XX PT Immunogens and vaccine comprising the immunogen useful for preventing and  
XX PT treating infectious diseases e.g. malaria and chronic disease e.g.  
XX PT cancer, comprises peptide and carrier from protein D of influenzae.  
XX PS Claim 9; Page 37; 53pp; English.  
XX CC The present invention describes an immunogen (I) comprising a peptide  
CC (1a) and a carrier (1b) derived from protein D of Haemophilus influenzae

CC or its fragment. Also described are: (1) a vaccine comprising (I), and an  
CC excipient; (2) preparation of (I), comprising conjugating a peptide to  
CC protein D or its fragment; and (3) preparation of a vaccine of (1),  
CC comprising formulating (I) with an excipient. (I) has cytostatic,  
CC anti-allergic, nocrotropic, neuroprotective and protozoacide activities. (I)  
CC and the vaccine are useful for the manufacture of a medicament for  
CC preventing and treating infectious diseases such as malaria or chronic  
CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
CC Unlike prior art immunogens, (I) induces high levels of antipeptide  
CC immune responses while inducing a moderate humoral response against the  
CC carrier. The present sequence represents a specifically claimed  
CC immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can be  
CC used in an immunogen of the present invention  
CC XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 47; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVD 9  
DB 1 EDGQVMDVD 9  
RESULT 3  
AAB51023  
ID AAB51023 standard; peptide; 9 AA.  
XX AAB51023;  
XX AC 21-MAR-2001 (first entry)  
XX DT IGE peptide #1.  
XX DE Vaccine; immunoglobulin E; IGE; anti-allergy.  
XX KW Mammalia.  
XX OS WO200074716-A2.  
XX PN 14-DEC-2000.  
XX PD 06-JUN-2000; 2000WO-EP005164.  
XX PF 08-JUN-1999; 99GB-00013327.  
XX PR (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX PA Prietels J;  
XX PI WPI; 2001-091150/10.  
XX DR New vaccine comprising allergy peptides linked by an inert carrier,  
XX PT useful for boosting an anti-allergy immune response in an individual  
XX PT susceptible to an allergic response.  
XX PS Claim 5; Page 20; 26pp; English.  
XX CC The present invention relates to a composition comprising allergy  
XX CC peptides linked by an inert carrier. The allergy peptides are derived  
XX CC from immunoglobulin E (IgE) or IGE receptor. The present peptide is one  
XX CC such peptide from IgE. The composition is useful as a vaccine or for  
XX CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
XX CC In particular, for boosting an anti-allergy immune response in an  
XX CC individual susceptible to an allergic response  
XX XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 47; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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PR 21-FEB-2002; 2002US-00080239.
PR 21-FEB-2002; 2002US-00082014.
XX (PAGE/) PAGE M.
PA (FRIE/) FRIEDE M.
XX Page M, Friele M;
XX WPI; 2003-852775/79.
XX Treating chronic hepatitis B infection by administering a T cell-
PT stimulating vaccine containing immunogenic particles having recombinant
PT carboxy-terminal truncated hepatitis B core (HBC) chimeric protein
PT molecules.
XX Disclosure; SEQ ID NO 127; 11pp; English.
XX The invention describes a method of treating chronic hepatitis comprising
CC administering to a patient a T cell-stimulating amount of a vaccine
CC comprising immunogenic particles dissolved or dispersed in a diluent,
CC where the immunogenic particles consists of recombinant hepatitis B core
CC (HBC) chimeric protein molecules, and maintaining the patient to induce T
CC cells activated against HBC. The methods and compositions of the present
CC invention are useful for treating chronic hepatitis B infection. This is
CC the amino acid sequence of a chimeric hepatitis B virus related B-cell
CC epitope useful for expression within the HBV chimera at the N-terminus,
CC within the immunogenic loop and/or at the C-terminus.
XX Sequence 9 AA:
SQ
Query Match 100.0%; Score 47; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EDGQVMDVD 9
Db 1 EDGQVMDVD 9
RESULT 7
AAE35091
XX AAE35091 standard; peptide; 9 AA.
XX AAE35091;
XX 28-MAY-2003 (first entry)
XX Human immunoglobulin E (IGE) HLA-A2 peptide motif #29.
XX Cytoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;
XX lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;
XX psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;
XX inflammatory bowel disease; insulin dependent diabetes; cell therapy;
XX Crohn's disease; allergic rhinitis; graft versus host disease; asthma;
XX transplant rejection; human; immunoglobulin E; IGE.
XX Homo sapiens.
XX WO200292773-A2.
XX 21-NOV-2002.
XX 13-MAY-2002; 2002WO-US015341.
XX 15-MAY-2001; 2001US-0291300P.
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;
XX WPI; 2003-120673/11.
XX Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases,
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PT comprises culturing CD8+ T cells with antigen presenting cells to
PT activate precursor CD8+ T cells specific for T the cell epitopes.
XX Example 3; Col 48; 49pp; English.
XX The invention relates to a method of producing cytotoxic T lymphocytes
XX (CTLs) specific for one or more non-tumour self antigen T cell epitopes.
CC The method involves loading antigen presenting cells (APCs) having class
CC I major histocompatibility complex molecules with the T cell epitopes,
CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+ T
CC cells specific for the T cell epitopes. The invention is useful for
CC treating autoimmune disease including rheumatoid arthritis, psoriasis,
CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,
CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,
CC graft versus host disease and transplant rejection and/or allergic
CC disease such as food allergy, hay fever, allergic rhinitis, allergic
CC asthma and venom allergy. The invention is also useful in cell therapy.
CC The present sequence is human immunoglobulin E (IGE) HLA-A2 peptide
XX motif. This peptide is used in the exemplification of the invention
XX Sequence 9 AA:
SQ
Query Match 66.0%; Score 31; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EDGQVM 6
Db 4 EDGQVM 9
RESULT 8
AAB25923
XX AAB25923 standard; peptide; 7 AA.
XX AAB25923;
XX 05-JAN-2001 (first entry)
XX P1 mimotope peptide P15s SEQ ID NO:17.
XX Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;
XX allergic disease; immunophylaxis; immunotherapy; antiallergic;
XX immunosuppressive; vaccine; histamine release inhibitor; immunogen;
XX allergy; atopy.
XX Homo sapiens.
XX WO200050460-A1.
XX 31-AUG-2000.
XX 22-FEB-2000; 2000WO-EP001455.
XX 25-FEB-1999; 99GB-00004405.
XX 23-MAR-1999; 99GB-00007151.
XX 07-MAY-1999; 99GB-00010537.
XX 07-MAY-1999; 99GB-00010538.
XX 07-AUG-1999; 99GB-00018594.
XX 07-AUG-1999; 99GB-00018603.
XX 07-SEP-1999; 99GB-00021046.
XX 07-SEP-1999; 99GB-00021047.
XX 29-OCT-1999; 99GB-00025619.
XX 23-NOV-1999; 99GB-00027698.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
XX Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Bassolsc;
XX WPI; 2000-572073/53.
```

PT Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.

PS Example 7; Page 35; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IGE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (1); (2) a vaccine (III)  
CC for treating allergies comprising (1); (3) a ligand (IV) capable of  
CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (1a) capable of being recognised by (IV); (6) an immunogen  
CC (IIa) comprising (1a) and (7) producing (III) by producing (II). (I) can  
CC have anti-allergic and immunosuppressive activities, and can be used as a  
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
CC in medicine and in the manufacture of medicaments for treating and  
CC preventing allergies. (IV) is useful for identifying mimotopes of PI, in  
CC medicine and also in manufacturing medicaments for treating allergies.  
CC (I) is useful in diagnostics and in the affinity purification of  
CC circulating anti-IGE antibodies from blood. (I), (III) and PC are useful  
CC for treating a patient susceptible to or suffering from allergies. (IV)  
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 63.8%; Score 30; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
| | | | |  
Db 1 QVMDVD 6

RESULT 9  
AAU16648  
ID AAU16648 standard; peptide; 7 AA.  
XX  
AC AAU16648;

DT 07-NOV-2001 (first entry)

DE Peptide P155 derived as mimotope of Cepsilon2 region of human IGE.

XX Human; linkage technology; conjugated compound; carrier vehicle; epitope;  
KW Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGE mediated disease;  
KW antibody response.

XX Homo sapiens.  
OS Synthetic.

PN WO200145745-A2.

PD 28-JUN-2001.

PF 21-DEC-2000; 2000WO-GB004935.

PR 21-DEC-1999; 99GB-00030233.

PR 22-FEB-2000; 2000GB-0004096.

PR 22-AUG-2000; 2000GB-00020707.

XX (ACAM-) ACAMBIS RES LTD.  
PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Flinn N, Johnson T;

DR WPI; 2001-521967/57.

PT A linkage comprising an immunogenic conjugate useful treatment of Ige

PT mediated diseases.

PS Example 4; Page 21; 48pp; English.

XX The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.  
CC macromolecules, polymers, dendrimers, proteins) to produce biological  
CC immunological constructs. The invention provides a method for linking an  
CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a  
CC pharmaceutical composition or a vaccine. The invention describes peptides  
CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4  
CC regions of human immunoglobulin E (IGE) which are used to produce  
CC conjugated compounds. The compounds or compositions of the invention are  
CC useful in the manufacture of a medicament for the treatment of IGE  
CC mediated diseases. The invention allows for controlled conjugation of a  
CC peptide epitope (antigen) to a protein so as to form an immunogenic  
CC conjugate which may be able to raise a protective antibody response in an  
CC animal or human patient. AAU1632-AAU1693 represent peptides derived  
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human  
CC IGE

XX Sequence 7 AA;

Query Match 63.8%; Score 30; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
| | | | |  
Db 1 QVMDVD 6

RESULT 10  
ABJ00227  
ID ABJ00227 standard; peptide; 7 AA.  
XX  
AC ABJ00227;

DT 02-SEP-2002 (first entry)

DE Human IGE immunogenic peptide SEQ ID NO: 11.

XX Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;  
KW vaccine; anti-allergic.

XX Homo sapiens.

PN WO200216409-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-EP009576.

PR 22-AUG-2000; 2000GB-00020717.

XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Friede M, Mason S, Tunnell WG, Vinals Y Bassolsc;

DR WPI; 2002-489648/52.

PT Conjugate for use in vaccine for treatment of allergy, comprises  
PT disulfide bridge cyclized peptide and immunogenic carrier.

PS Claim 4; Page 9; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention

SQ Sequence 7 AA;

Query Match 63.8%; Score 30; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 |||||  
 Db 1 QVMDVD 6

RESULT 11  
 AAE35076  
 ID AAE35076 standard; peptide; 9 AA.  
 AC AAE35076;  
 XX  
 XX 28-MAY-2003 (first entry)  
 DE Human immunoglobulin E (IgE) HLA-A2 peptide motif #14.  
 XX  
 XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
 KM lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
 KM psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
 KM inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
 KM Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
 KM transplant rejection; human; immunoglobulin E; IgE.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200292773-A2.  
 PN  
 XX 21-NOV-2002.  
 PD  
 XX 13-MAY-2002; 2002MO-US015341.  
 PF  
 XX 15-MAY-2001; 2001US-0291300P.  
 PR  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA  
 XX Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;  
 PI  
 XX WPI; 2003-120673/11.  
 DR  
 XX Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases,  
 PT comprising culturing CD8+ T cells with antigen presenting cells to  
 PT activate precursor CD8+ T cells specific for T cell epitopes.  
 XX  
 XX Example 3; Col 47; 49pp; English.  
 PS  
 XX The invention relates to a method of producing cytotoxic T lymphocytes  
 XX (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
 CC The method involves loading antigen presenting cells (APCs) having class  
 CC I major histocompatibility complex molecules with the T cell epitopes, T  
 CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+ T  
 CC cells specific for the T cell epitopes. The invention is useful for  
 CC treating autoimmune diseases including rheumatoid arthritis, psoriasis,  
 CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
 CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
 CC graft versus host disease and transplant rejection and/or allergic  
 CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
 CC asthma and venom allergy. The invention is also useful in cell therapy.  
 CC The present sequence is human immunoglobulin E (IgE) HLA-A2 peptide  
 CC motif. This peptide is used in the exemplification of the invention  
 CC  
 XX  
 XX Sequence 9 AA;

Query Match 63.8%; Score 30; DB 6; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 |||||

Db 1 QVMDVD 6

RESULT 12  
 AAE14481  
 ID AAE14481 standard; peptide; 7 AA.  
 XX  
 XX AAE14481;  
 AC  
 XX 07-AUG-2003 (revised)  
 DT 26-MAR-2002 (first entry)  
 XX  
 XX Oplophorus gracilirostris luciferase 35 kDa subunit peptide.  
 DE  
 XX Luciferase; deep sea luminous shrimp; decapoda; reporter enzyme;  
 KM 35 kDa subunit; photoprotein.  
 XX  
 XX Oplophorus gracilirostris.  
 OS  
 XX EP1156103-A2.  
 PN  
 XX 21-NOV-2001.  
 PD  
 XX 25-APR-2001; 2001EP-00109479.  
 PF  
 XX 26-APR-2000; 2000JP-00125053.  
 PR  
 XX (CHCC ) CHISSO CORP.  
 PA  
 XX Inouye S;  
 PI  
 XX WPI; 2002-084319/12.  
 DR  
 XX Novel secretional luciferase derived from the deep sea luminous shrimp  
 PT Oplophorus gracilirostris consists of 19kDa and 35 kDa subunits and is  
 PT useful as a reporter enzyme.  
 XX  
 XX Example 4; Page 11; 35pp; English.  
 PS  
 XX The invention relates to polynucleotide encoding secretional luciferase  
 CC derived from deep sea luminous shrimp (Oplophorus gracilirostris). The  
 CC luciferase protein is composed of 19 and 35 kDa proteins and is useful as  
 CC a reporter enzyme. Antibodies against luciferase and oligonucleotides  
 CC derived from luciferase polynucleotides are useful for identification of  
 CC novel luciferase or photoproteins from related species. The present  
 CC sequence is a peptide from 35 kDa subunit of Oplophorus gracilirostris  
 CC luciferase. (Updated on 07-AUG-2003 to correct OS field.)  
 CC  
 XX  
 XX Sequence 7 AA;

Query Match 59.6%; Score 28; DB 5; Length 7;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QVMDVD 9  
 |||||  
 Db 1 QVMDVD 7

RESULT 13  
 ABJ12821  
 ID ABJ12821 standard; peptide; 9 AA.  
 XX  
 XX ABJ12821;  
 AC  
 XX 10-DEC-2002 (first entry)  
 DT  
 XX Human 125P5C8 epitope #1447.  
 DE  
 XX Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
 KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
 XX  
 XX Homo sapiens.  
 OS

XX XX WO200272785-A2.  
EN  
XX  
PD 19-SEP-2002.  
XX  
PF 13-MAR-2002; 2002WO-US007855.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PA (AGEN-) AGENSYS INC.  
PI Fatis M, Chalilila-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
PI Morrison RK, Morrison K, Jakobovits A;  
XX WPI; 2002-713510/77.  
XX  
XX New composition comprising a substance that modulates the status of  
PT 12SP5C8 gene or a molecule that is modulated by 12SP5C8, useful for  
PT treating or preventing cancer that expresses or over expresses 12SP5C8.  
XX  
XX Disclosure; Page 163; 274pp; English.  
PS  
XX The present invention relates to compositions comprising a substance that  
CC modulates the status of 12SP5C8 or a molecule that is modulated by  
CC 12SP5C8. The status of a cell that expresses 12SP5C8 is modulated. The  
CC composition is useful for treating cancer, particularly prostate,  
CC bladder, kidney, colon, ovary or breast cancer. The 12SP5C8 protein  
CC and/or a nucleotide sequence encoding the protein is useful for  
CC immunising a mammal against cancer. The present sequence is a 12SP5C8  
CC epitope shown in the exemplification of the invention  
XX  
SQ Sequence 9 AA;  
Query Match 59.6%; Score 28; DB 5; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 EDGQVMDVD 9  
Db 1 EHGNVKIDID 9  
RESULT 14  
AAE35101  
ID AAE35101 standard; peptide; 9 AA.  
XX  
AC AAE35101;  
XX  
DT 28-MAY-2003 (first entry)  
XX  
DE Human immunoglobulin E (Ige) HLA-A2 peptide motif #39.  
XX  
XX Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;  
KM lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;  
KM psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;  
KM inflammatory bowel disease; insulin dependent diabetes; cell therapy;  
KM Crohn's disease; allergic rhinitis; graft versus host disease; asthma;  
KM transplant rejection; human; immunoglobulin E; Ige.  
XX  
OS Homo sapiens.  
XX  
PN WO200292773-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 13-MAY-2002; 2002WO-US015341.  
XX  
PR 15-MAY-2001; 2001US-0291300P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
PI Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;  
XX

DR WPI; 2003-120673/11.  
XX  
XX Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases,  
PT comprises culturing CD8+ T cells with antigen presenting cells to  
PT activate precursor CD8+ T cells specific for T cell epitopes.  
XX  
PS Example 3; Col 48; 49pp; English.  
XX  
XX The invention relates to a method of producing cytotoxic T lymphocytes  
CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.  
CC The method involves loading antigen presenting cells (APCs) having class  
CC I major histocompatibility complex molecules with the T cell epitopes,  
CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+ T  
CC cells specific for the T cell epitopes. The invention is useful for  
CC treating autoimmune disease including rheumatoid arthritis, psoriasis,  
CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,  
CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,  
CC graft versus host disease and transplant rejection and/or allergic  
CC disease such as food allergy, hay fever, allergic rhinitis, allergic  
CC asthma and venom allergy. The invention is also useful in cell therapy.  
CC The present sequence is human immunoglobulin E (Ige) HLA-A2 peptide  
CC motif. This peptide is used in the exemplification of the invention  
XX  
SQ Sequence 9 AA;  
Query Match 55.3%; Score 26; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQV 5  
Db 5 EDGQV 9  
RESULT 15  
ABG67564  
ID ABG67564 standard; peptide; 9 AA.  
XX  
AC ABG67564;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Human ADPI tryptic digest peptide #273.  
XX  
XX Human; Alzheimer's disease; AD; brain tissue; ADP; ADPI;  
KM Alzheimer's disease-associated feature; neuroprotective;  
KM Alzheimer's disease-associated protein isoform; nootropic;  
KM ADPI tryptic digest peptide.  
XX  
OS Homo sapiens.  
XX  
PN WO200246767-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 29-NOV-2001; 2001WO-GB005289.  
XX  
PR 08-DEC-2000; 2000US-0254431P.  
XX  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
PI Herath HMA, Parekh RB, Rohlf C;  
XX  
DR WPI; 2002-508575/54.  
XX  
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
PT comprises detecting Alzheimer disease-associated features or Alzheimer  
PT disease-associated protein isoforms in brain tissue from the subject.  
XX  
PS Claim 7; Page 58; 427pp; English.  
XX  
XX The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a

CC subject. The method comprises analysing a sample of brain tissue from a  
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
 CC disease-associated features (ADFs), whose relative abundance correlates  
 CC with the presence, absence, stage or severity of AD and comparing the  
 CC abundance of each feature with the abundance of that chosen feature in  
 CC brain tissue from persons free from AD. The invention also describes  
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
 CC brain tissue. The methods and compositions of the invention are useful  
 CC for the screening, diagnosis or prognosis of AD in a subject, for  
 CC determining the stage or severity of AD in a subject, for identifying a  
 CC subject at risk of developing AD, or for monitoring the effect of therapy  
 CC administered to a subject having AD. Antibodies capable of binding to  
 CC ADPIs are useful for treating or preventing AD, and for determining the  
 CC efficacy of a given treatment regime. An agent that modulates the  
 CC activity of ADPI is useful in the manufacture of a medicament for the  
 CC treatment or prevention of AD in a subject. AB667292-AB668038 represent  
 CC human ADPI tryptic digest peptides  
 XX

SQ Sequence 9 AA;

Query Match 53.2%; Score 25; DB 5; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQWMDV 8  
 |||||  
 Db 1 GQVFDV 6

Search completed: August 23, 2004, 10:53:32  
 Job time : 124 secs

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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:56:07 ; Search time 120 seconds

(without alignments)  
23.566 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDGQVMDVD 9

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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 9

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Maximum Match 100%  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	12	US-10-362-527-1
2	47	100.0	9	14	US-10-082-014-273
3	47	100.0	9	14	US-10-372-076-127
4	47	100.0	9	16	US-10-677-074-127
5	30	69.8	7	12	US-10-362-527-11
6	30	59.6	7	9	US-09-842-164-12
7	28	59.6	7	15	US-10-377-714-12
8	25	53.2	9	12	US-10-014-340-291
9	23	48.9	9	14	US-10-147-140-47
10	23	48.9	9	16	US-10-415-014-305
11	23	48.9	9	16	US-10-415-014-305
12	22	46.8	7	9	US-09-884-767A-110
13	22	46.8	7	14	US-10-006-869-1617
14	22	46.8	7	15	US-10-395-032-1617
15	22	46.8	8	14	US-10-006-869-1623

16	22	46.8	8	15	US-10-395-032-1623	Sequence 1623, Ap
17	22	46.8	9	10	US-09-820-649-263	Sequence 263, Ap
18	22	46.8	9	14	US-10-006-869-1626	Sequence 1626, Ap
19	22	46.8	9	14	US-10-160-162-263	Sequence 263, Ap
20	22	46.8	9	15	US-10-395-032-1626	Sequence 1626, Ap
21	21	44.7	8	10	US-09-993-180-28	Sequence 28, Ap
22	21	44.7	9	9	US-09-780-053-142	Sequence 57, Ap
23	21	44.7	9	9	US-09-780-053-142	Sequence 142, Ap
24	21	44.7	9	9	US-09-780-053-142	Sequence 253, Ap
25	21	44.7	9	9	US-09-780-053-142	Sequence 434, Ap
26	21	44.7	9	9	US-09-780-053-142	Sequence 454, Ap
27	21	44.7	9	9	US-09-780-053-142	Sequence 556, Ap
28	21	44.7	9	9	US-09-920-174-41	Sequence 41, Ap
29	21	44.7	9	10	US-09-920-174-41	Sequence 41, Ap
30	21	44.7	9	12	US-10-253-286-474	Sequence 474, Ap
31	21	44.7	9	15	US-10-245-871-474	Sequence 474, Ap
32	21	44.7	9	16	US-10-365-761B-5	Sequence 5, Ap
33	21	44.7	9	16	US-10-447-161-75	Sequence 75, Ap
34	21	44.7	9	16	US-10-258-144-8	Sequence 8, Ap
35	20	42.6	6	10	US-09-931-325A-105	Sequence 105, Ap
36	20	42.6	6	10	US-09-930-915A-245	Sequence 245, Ap
37	20	42.6	6	16	US-10-806-006-245	Sequence 245, Ap
38	20	42.6	6	16	US-10-805-913-245	Sequence 245, Ap
39	20	42.6	8	12	US-10-149-135-176	Sequence 176, Ap
40	20	42.6	8	12	US-10-149-135-176	Sequence 306, Ap
41	20	42.6	8	12	US-10-149-135-176	Sequence 589, Ap
42	20	42.6	8	12	US-10-149-135-176	Sequence 666, Ap
43	20	42.6	8	12	US-10-149-135-176	Sequence 1121, Ap
44	20	42.6	8	12	US-10-149-135-176	Sequence 1196, Ap
45	20	42.6	8	12	US-10-149-135-176	Sequence 1373, Ap

#### ALIGNMENTS

RESULT 1  
US-10-362-527-1  
Sequence 1, Application US/10362527  
Publication No. US20040030106A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
TITLE OF INVENTION: and use thereof in the treatment of Allergies  
FILE REFERENCE: B45236  
CURRENT APPLICATION NUMBER: US/10/362,527  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: PCT/EP01/09576  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: GB 0020717.5  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-362-527-1  
Query Match 100.0%; Score 47; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 EDGQVMDVD 9  
Db 1 EDGQVMDVD 9  
RESULT 2  
US-10-082-014-273  
Sequence 273, Application US/10082014

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Publication No. US2003018585A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
PRIORITY FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
PRIORITY FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.1
SEQ ID NO 273
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-082-014-273

Query Match      100.0%; Score 47; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
        |||||
        1 EDGQVMDVD 9

Db

RESULT 3
US-10-372-076-127
Sequence 127, Application US/10372076
Publication No. US20030198645A1
GENERAL INFORMATION:
APPLICANT: Friede, Mark
APPLICANT: Friede, Martin
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/372,076
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.2
SEQ ID NO 127
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-372-076-127

Query Match      100.0%; Score 47; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
        |||||
        1 EDGQVMDVD 9

Db

RESULT 4
US-10-677-074-127
Sequence 127, Application US/10677074
Publication No. US20040156863A1
GENERAL INFORMATION:
APPLICANT: Friede, Mark
APPLICANT: Friede, Martin
APPLICANT: Schmidt, Annette Elisabeth
APPLICANT: Stober, Detlef
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/677,074
CURRENT FILING DATE: 2003-10-01
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PRIOR APPLICATION NUMBER: 10/372,076
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.2
SEQ ID NO 127
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-677-074-127

Query Match      100.0%; Score 47; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
        |||||
        1 EDGQVMDVD 9

Db

RESULT 5
US-10-362-527-11
Sequence 11, Application US/10362527
Publication No. US20040030106A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnell, William Gordon
APPLICANT: Vinals Y De Bassols, Carlota
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
FILE REFERENCE: B45236
CURRENT APPLICATION NUMBER: US/10/362,527
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/EP01/09576
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: GB 0020717.5
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-10-362-527-11

Query Match      63.8%; Score 30; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 QVMDVD 9
        |||||
        1 QVMDVD 6

Db

RESULT 6
US-09-842-164-12
Sequence 12, Application US/09842164
Patent No. US20020102687A1
GENERAL INFORMATION:
APPLICANT: Inouye, Satoshi
TITLE OF INVENTION: Luciferase and Photoprotein
FILE REFERENCE: 206497US0
CURRENT APPLICATION NUMBER: US/09/842,164
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: JAPAN 2000-125053
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
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```

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Ophiophorus gracilirostris
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(7)
; OTHER INFORMATION: PRT, 35 kDa protein, partial
US-09-842-164-12

```

```

Query Match          59.6%; Score 28; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GQVMDVD 9
Db 1 GDVMDMD 7

```

```

RESULT 7
US-10-377-714-12
; Sequence 12, Application US/10377714
; Publication No. US20040002127A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, SATOSHI
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN
; FILE REFERENCE: 206497U50
; CURRENT APPLICATION NUMBER: US/10/377, 714
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US/09/842, 164A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 2000-125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Ophiophorus gracilirostris
US-10-377-714-12

```

```

Query Match          59.6%; Score 28; DB 15; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GQVMDVD 9
Db 1 GDVMDMD 7

```

```

RESULT 8
US-10-014-340-291
; Sequence 291, Application US/10014340
; Publication No. US2003006441A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014, 340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 291
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-291

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```

Query Match          53.2%; Score 25; DB 12; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GQVMDV 8

```

```

Db 1 GQVMDV 6

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RESULT 9
US-10-147-140-47
; Sequence 47, Application US/10147140
; Publication No. US20030153730A1
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY
; APPLICANT: LIOTTA, LANCE
; APPLICANT: SCHIFFMANN, ELLIOTT
; APPLICANT: KRUTZCH, HENRY
; APPLICANT: MURATA, JUN
; TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
; FILE REFERENCE: 2026-4149US4
; CURRENT APPLICATION NUMBER: US/10/147, 140
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 07/822, 043
; PRIOR FILING DATE: 1992-01-17
; PRIOR APPLICATION NUMBER: 08/249, 182
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/346, 455
; PRIOR FILING DATE: 1994-11-28
; PRIOR APPLICATION NUMBER: 08/977, 221
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-147-140-47

```

```

Query Match          48.9%; Score 23; DB 14; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GQVMD 7
Db 3 GQVMD 7

```

```

RESULT 10
US-10-415-014-220
; Sequence 220, Application US/10415014
; Publication No. US20040110674A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairis, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158200400
; CURRENT APPLICATION NUMBER: US/10/415, 014
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: PCT/US02/27760
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/316, 664
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-014-220

```

Query Match 48.9%; Score 23; DB 16; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 |::|||  
 Db 2 QUIDVD 7

RESULT 11  
 US-10-415-014-305  
 ; Sequence 305, Application US/10415014  
 ; Publication No. US20040110674A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chailita-Eld, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Faris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN  
 ; TITLE OF INVENTION: ENTITLED 205P1B5 USEFUL IN TREATMENT AND DETECTION OF CANCER  
 ; FILE REFERENCE: 511582004300  
 ; CURRENT APPLICATION NUMBER: US/10/415,014  
 ; CURRENT FILING DATE: 2003-11-19  
 ; PRIOR APPLICATION NUMBER: PCT/US02/27760  
 ; PRIOR FILING DATE: 2002-08-30  
 ; PRIOR APPLICATION NUMBER: US 60/316,664  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 736  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 305  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-415-014-305

US-10-415-014-305

Query Match 48.9%; Score 23; DB 16; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 |::|||  
 Db 2 QUIDVD 7

RESULT 12

US-09-884-767A-110  
 ; Sequence 110, Application US/09884767A  
 ; Publication No. US20020192789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DYAX Corp.  
 ; APPLICANT: Ley, Arthur C.  
 ; APPLICANT: Luneau, Christopher J.  
 ; APPLICANT: Ladner, Robert C.  
 ; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
 ; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
 ; CURRENT APPLICATION NUMBER: US/09/884,767A  
 ; CURRENT FILING DATE: 2001-06-19  
 ; PRIOR APPLICATION NUMBER: US 09/597,321  
 ; PRIOR FILING DATE: 2000-06-19  
 ; NUMBER OF SEQ ID NOS: 217  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 110  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
 ; US-09-884-767A-110

Query Match 46.8%; Score 22; DB 9; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+06;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QVMDVD 7  
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 Db 1 QUIDVD 5

RESULT 13  
 US-10-006-869-1617  
 ; Sequence 1617, Application US/10006869  
 ; Publication No. US20030082166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Symonds, James Matthew  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
 ; FILE REFERENCE: 100086.407C7  
 ; CURRENT APPLICATION NUMBER: US/10/006,869  
 ; CURRENT FILING DATE: 2001-12-03  
 ; NUMBER OF SEQ ID NOS: 4052  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1617  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Representative cyclic modulating agent based on  
 ; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
 ; US-10-006-869-1617

Query Match 46.8%; Score 22; DB 14; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 |::|||  
 Db 2 QUIDVD 7

RESULT 14

US-10-395-032-1617  
 ; Sequence 1617, Application US/10395032  
 ; Publication No. US20030229199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Symonds, James Matthew  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
 ; FILE REFERENCE: 100086.407C9  
 ; CURRENT APPLICATION NUMBER: US/10/395,032  
 ; CURRENT FILING DATE: 2003-03-21  
 ; NUMBER OF SEQ ID NOS: 4052  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1617  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Representative cyclic modulating agent based on  
 ; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
 ; US-10-395-032-1617

Query Match 46.8%; Score 22; DB 15; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 |::|||  
 Db 2 QUIDVD 7

RESULT 15  
 US-10-006-869-1623  
 ; Sequence 1623, Application US/10006869  
 ; Publication No. US20030082166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Symonds, James Mathew  
 ; APPLICANT: Gour, Bardara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
 ; FILE REFERENCE: 100086.407C7  
 ; CURRENT APPLICATION NUMBER: US/10/006,869  
 ; NUMBER OF SEQ ID NOS: 4052  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1623  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Representative cyclic modulating agent based on  
 ; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
 US-10-006-869-1623

Query Match 46.8%; Score 22; DB 14; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVMDVD 9  
 | : |||  
 Db 3 QINDVD 8

Search completed: August 23, 2004, 11:07:22  
 Job time : 121 secs

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OM protein - protein search, using sw model

Run on: August 23, 2004, 10:54:07 ; Search time 57 Seconds

(without alignments)  
19.204 Million cell updates/sec

Title: US-09-914-088-1

Perfect score: 47

Sequence: 1 EDGQVMDVD 9

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 673640 seqs, 121625480 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	1	PCT-US04-05047-127
2	47	100.0	9	1	PCT-US03-39164A-141
3	47	100.0	9	6	US-10-732-862A-141
4	22	46.8	8	6	US-10-111-983-653
5	22	46.8	8	6	US-10-111-983-14911
6	22	46.8	8	6	US-10-111-983-26906
7	22	46.8	9	6	US-10-693-657-48
8	21	44.7	8	6	US-10-712-425-722
9	21	44.7	8	6	US-10-059-447B-3
10	21	44.7	9	1	PCT-IL03-00501A-44
11	21	44.7	9	6	US-10-111-983-10642
12	21	44.7	9	6	US-10-752-380-41
13	20	42.6	6	1	PCT-US03-39164A-411
14	20	42.6	6	6	US-10-732-862A-411
15	20	42.6	6	6	US-10-805-913-245
16	20	42.6	6	6	US-10-806-006-245
17	20	42.6	7	6	US-10-111-983-1135
18	20	42.6	7	6	US-10-111-983-15379
19	20	42.6	7	6	US-10-111-983-27391
20	20	42.6	7	6	US-10-111-983-28603
21	20	42.6	8	5	US-09-458-298B-176
22	20	42.6	8	5	US-09-458-298B-306
23	20	42.6	8	5	US-09-458-298B-589
24	20	42.6	8	5	US-09-458-298B-666
25	20	42.6	8	5	US-09-458-298B-1121
26	20	42.6	8	5	US-09-458-298B-1196

27	20	42.6	8	5	US-09-458-298B-1373	Sequence 1373, Ap
28	20	42.6	8	5	US-09-458-298B-1699	Sequence 1699, Ap
29	20	42.6	8	5	US-09-633-364C-371	Sequence 371, App
30	20	42.6	8	5	US-09-633-364C-2668	Sequence 2668, App
31	20	42.6	8	5	US-09-350-401B-598	Sequence 598, App
32	20	42.6	8	5	US-09-350-401B-2181	Sequence 2181, App
33	20	42.6	8	5	US-09-350-401B-2502	Sequence 2502, Ap
34	20	42.6	8	5	US-09-350-401B-2566	Sequence 2566, Ap
35	20	42.6	8	5	US-09-350-401B-2749	Sequence 2749, Ap
36	20	42.6	8	6	US-10-111-983-5891	Sequence 5891, Ap
37	20	42.6	8	6	US-10-111-983-5915	Sequence 5915, Ap
38	20	42.6	8	6	US-10-111-983-19850	Sequence 19850, A
39	20	42.6	8	6	US-10-111-983-31905	Sequence 31905, A
40	20	42.6	8	6	US-10-654-601-1822	Sequence 1822, App
41	20	42.6	8	6	US-10-654-601-1563	Sequence 1563, App
42	20	42.6	9	1	PCT-US03-38949-731	Sequence 731, App
43	20	42.6	9	5	US-09-458-298B-135	Sequence 135, App
44	20	42.6	9	5	US-09-458-298B-559	Sequence 559, App
45	20	42.6	9	5	US-09-458-298B-1102	Sequence 1102, Ap

## ALIGNMENTS

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RESULT 1
PCT-US04-05047-127
; Sequence 127, Application PC/TUS0405047
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; APPLICANT: Schmidt, Annette Elisabeth
; APPLICANT: Stober, Detlef
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/91569
; CURRENT APPLICATION NUMBER: PCT/US04/05047
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 10/677,074
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 10/372,076
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-05047-127

Query Match          100.0%; Score 47; DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 2
PCT-US03-39164A-141
; Sequence 141, Application PC/TUS0339164A
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelynne J.
; APPLICANT: Jay, Aaron J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136-0PCT (4564-91156)
; CURRENT APPLICATION NUMBER: PCT/US03/39164A
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US03/05196
; PRIOR FILING DATE: 2003-02-20
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NUMBER OF SEQ ID NOS: 455  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 141  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US03-39164A-141

Query Match  
Best Local Similarity 100.0%; Score 47; DB 1; Length 9;  
Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 EDGQVMDVD 9  
Db 1 EDGQVMDVD 9

RESULT 3  
US-10-732-862A-141  
Sequence 141, Application US/10732862A  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, BIRKETT J.  
APPLICANT: Lyons, Katelynne J.  
APPLICANT: Jay, Haron J.  
TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES  
FILE REFERENCE: ICC-136.0 (4564-88881)  
CURRENT APPLICATION NUMBER: US/10/732,862A  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 60/432,123  
PRIOR FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: US 10/274,616  
PRIOR FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 141  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-732-862A-141

Query Match  
Best Local Similarity 100.0%; Score 47; DB 6; Length 9;  
Pred. No. 6e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 EDGQVMDVD 9  
Db 1 EDGQVMDVD 9

RESULT 4  
US-10-111-983-653  
Sequence 653, Application US/10111983  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: GALEOTTI Cesira  
APPLICANT: GRANDI Guido  
APPLICANT: MASIGNANI Vega  
APPLICANT: MORA Mariaros  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: RAPPUOLI Rino  
APPLICANT: RATTI Giulio  
APPLICANT: SCARLATO Vincenzo  
APPLICANT: SCARSELLI Maria  
TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES  
FILE REFERENCE: 2300-1654 (PP01654.003)  
CURRENT APPLICATION NUMBER: US/10/111,983  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US-60/162616  
PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 37764  
SOFTWARE: SeqWin99, version 1.02  
SEQ ID NO 653  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Neisseria  
US-10-111-983-653

Query Match  
Best Local Similarity 46.8%; Score 22; DB 6; Length 8;  
Pred. No. 6e+05; Mismatches 1; Indels 0; Gaps 0;  
Matches 4; Conservative 3;

QY 2 DGQVMDVD 9  
Db 1 NGKRVMDVD 8

RESULT 5  
US-10-111-983-14911  
Sequence 14911, Application US/10111983  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: GALEOTTI Cesira  
APPLICANT: GRANDI Guido  
APPLICANT: MASIGNANI Vega  
APPLICANT: MORA Mariaros  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: RAPPUOLI Rino  
APPLICANT: RATTI Giulio  
APPLICANT: SCARLATO Vincenzo  
APPLICANT: SCARSELLI Maria  
TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES  
FILE REFERENCE: 2300-1654 (PP01654.003)  
CURRENT APPLICATION NUMBER: US/10/111,983  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US-60/162616  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 37764  
SOFTWARE: SeqWin99, version 1.02  
SEQ ID NO 14911  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Neisseria  
US-10-111-983-14911

Query Match  
Best Local Similarity 46.8%; Score 22; DB 6; Length 8;  
Pred. No. 6e+05; Mismatches 1; Indels 0; Gaps 0;  
Matches 4; Conservative 3;

QY 2 DGQVMDVD 9  
Db 1 NGKRVMDVD 8

RESULT 6  
US-10-111-983-26906  
Sequence 26906, Application US/10111983  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: GALEOTTI Cesira  
APPLICANT: GRANDI Guido  
APPLICANT: MASIGNANI Vega  
APPLICANT: MORA Mariaros  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: RAPPUOLI Rino  
APPLICANT: RATTI Giulio  
APPLICANT: SCARLATO Vincenzo  
APPLICANT: SCARSELLI Maria  
TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES  
FILE REFERENCE: 2300-1654 (PP01654.003)  
CURRENT APPLICATION NUMBER: US/10/111,983  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US-60/162616

;; PRIOR FILING DATE: 1999-10-29  
;; NUMBER OF SEQ ID NOS: 37764  
;; SOFTWARE: SeqMan99, version 1.02  
;; SEQ ID NO: 26906  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Neisseria  
US-10-111-983-26906

Query Match  
Best Local Similarity 46.8%; Score 22; DB 6; Length 8;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGVQVMDVD 9  
Db 1 NGKRVVD 8

RESULT 7  
US-10-693-657-48  
;; Sequence 48, Application US/10693657  
;; GENERAL INFORMATION:  
;; APPLICANT: Chemcob, Sylvain  
;; APPLICANT: Martin, Beauchamp  
;; APPLICANT: Quinloun, Christiane  
;; TITLE OF INVENTION: Cytokine receptors modulators, method of identifying same, and  
;; FILE REFERENCE: GOND:040US  
;; CURRENT APPLICATION NUMBER: US/10/693,657  
;; CURRENT FILING DATE: 2003-10-24  
;; PRIOR APPLICATION NUMBER: 60/420,679  
;; PRIOR FILING DATE: 2002-10-24  
;; PRIOR APPLICATION NUMBER: 60/423,530  
;; PRIOR FILING DATE: 2002-11-05  
;; NUMBER OF SEQ ID NOS: 65  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 48  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURES:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-693-657-48

Query Match  
Best Local Similarity 46.8%; Score 22; DB 6; Length 9;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGVQVMDVD 9  
Db 2 NGSVIYD 9

RESULT 8  
US-10-712-425-722  
;; Sequence 722, Application US/10712425  
;; GENERAL INFORMATION:  
;; APPLICANT: LER, FRANK D.  
;; APPLICANT: MENG, XUN  
;; APPLICANT: LIVINGSTON, DAVID  
;; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN  
;; FILE REFERENCE: ENG-002-001  
;; CURRENT APPLICATION NUMBER: US/10/712,425  
;; CURRENT FILING DATE: 2003-11-13  
;; PRIOR APPLICATION NUMBER: 60/379,626  
;; PRIOR FILING DATE: 2002-05-10  
;; PRIOR APPLICATION NUMBER: 60/393,137  
;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/393,197  
;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/393,211

;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/393,223  
;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/393,233  
;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/393,235  
;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/393,280  
;; PRIOR FILING DATE: 2002-07-01  
;; PRIOR APPLICATION NUMBER: 60/430,948  
;; PRIOR FILING DATE: 2002-12-04  
;; PRIOR APPLICATION NUMBER: 60/433,319  
;; PRIOR FILING DATE: 2002-12-13  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 1386  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 722  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Human severe acute respiratory syndrome virus  
US-10-712-425-722

Query Match  
Best Local Similarity 44.7%; Score 21; DB 6; Length 8;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGVQVMDVD 9  
Db 1 DEELMELD 8

RESULT 9  
US-10-059-447B-3  
;; Sequence 3, Application US/10059447B  
;; GENERAL INFORMATION:  
;; APPLICANT: Smith, Daniel  
;; TITLE OF INVENTION: ALPHA-N-ACETYLGLACTOSAMINIDASE FROM CLOSTRIDIUM PERFRINGENS  
;; FILE REFERENCE: 0994.00134  
;; CURRENT APPLICATION NUMBER: US/10/059,447B  
;; CURRENT FILING DATE: 2002-01-29  
;; PRIOR APPLICATION NUMBER: 60/064,683  
;; PRIOR FILING DATE: 1997-11-03  
;; PRIOR APPLICATION NUMBER: 10/185,476  
;; PRIOR FILING DATE: 1998-11-03  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 3  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Clostridium perfringens  
US-10-059-447B-3

Query Match  
Best Local Similarity 44.7%; Score 21; DB 6; Length 8;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQSV 5  
Db 1 EDQSV 5

RESULT 10  
PCT-IL03-00501A-44  
;; Sequence 44, Application PC/TILO300501A  
;; GENERAL INFORMATION:  
;; APPLICANT: GAVISH-GALILEE BIO APPLICATIONS LTD.  
;; APPLICANT: GROSS, Gideon  
;; APPLICANT: MARGALIT, ALON  
;; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC CI  
;; FILE REFERENCE: GAVISH-004 PCT  
;; CURRENT APPLICATION NUMBER: PCT/IL03/00501A  
;; CURRENT FILING DATE: 2003-06-12

PRIOR APPLICATION NUMBER: US 60/388,273  
PRIOR FILING DATE: 2002-06-12  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 44  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
PCT-IL03-00501A-44

Query Match 44.7%; Score 21; DB 1; Length 9;  
Best Local Similarity 57.1%; Pred. No. 6e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DQVMDV 8  
Db 3 DQVMSL 9

RESULT 11  
US-10-111-983-10642  
Sequence 10642, Application US/10111983  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: GALEOTTI Cesira  
APPLICANT: GRANDI Guido  
APPLICANT: MASIGNANI Vega  
APPLICANT: MORA Mariarosa  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: RAPPUOLI Rino  
APPLICANT: RATTI Giulio  
APPLICANT: SCARLATO Vincenzo  
APPLICANT: SCARSELLI Maria  
TITLE OF INVENTION: NEISERIAL ANTIGENIC PEPTIDES  
FILE REFERENCE: 2300-1654 (PP01654.003)  
CURRENT APPLICATION NUMBER: US/10/111,983  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US-60/162616  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 37764  
SOFTWARE: SeqMan99, version 1.02  
SEQ ID NO 10642  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Neisseria  
US-10-111-983-10642

Query Match 44.7%; Score 21; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 6e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DQVMD 7  
Db 4 DQKTYD 9

RESULT 12  
US-10-752-380-41  
Sequence 41, Application US/10752380  
GENERAL INFORMATION:  
APPLICANT: KHANNA, RAJIV  
APPLICANT: KERR, BEVERLEY M.  
APPLICANT: MISKO, IHOR S.  
APPLICANT: MOSS, DENIS J.  
APPLICANT: BURROWS, SCOTT R.  
TITLE OF INVENTION: EBV CTL EPTOPES  
FILE REFERENCE: FRRC:008  
CURRENT APPLICATION NUMBER: US/10/752,380  
CURRENT FILING DATE: 2004-01-06  
PRIOR APPLICATION NUMBER: US/09/194,450  
PRIOR FILING DATE: 1999-06-25

NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 41  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-752-380-41

Query Match 44.7%; Score 21; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DQOV 5  
Db 4 DQOV 7

RESULT 13  
PCT-US03-39164A-411  
Sequence 411, Application PC/TUS0339164A  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, BIRKETT J.  
APPLICANT: LYONS, KATELYNNE J.  
APPLICANT: JAY, HARON J.  
TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES  
FILE REFERENCE: ICC-136.0PCT (4564-91156)  
CURRENT APPLICATION NUMBER: PCT/US03/39164A  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 60/432,123  
PRIOR FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: PCT/US03/05196  
PRIOR FILING DATE: 2003-02-20  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 411  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: primer protein seugence  
PCT-US03-39164A-411

Query Match 42.6%; Score 20; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 6e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MDVD 9  
Db 1 MDID 4

RESULT 14  
US-10-732-862A-411  
Sequence 411, Application US/10732862A  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, BIRKETT J.  
APPLICANT: LYONS, KATELYNNE J.  
APPLICANT: JAY, HARON J.  
TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES  
FILE REFERENCE: ICC-136.0 (4564-88881)  
CURRENT APPLICATION NUMBER: US/10/732,862A  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: US 60/432,123  
PRIOR FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: US 10/274,616  
PRIOR FILING DATE: 2002-10-21  
PRIOR APPLICATION NUMBER: US 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: US 10/082,014  
PRIOR FILING DATE: 2002-02-22



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; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 411
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer protein seugence
US-10-732-862A-411

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Query Match          42.6%; Score 20; DB 6; Length 6;
Best Local Similarity 75.0%; Pred. No. 6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY      6 MDVD 9
        ||:|
Db      1 MDID 4

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RESULT 15
US-10-805-913-245
; Sequence 245, Application US/10805913
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/91645 ICC-102.2 DV II
; CURRENT APPLICATION NUMBER: US/10/805,913
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 245
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-805-913-245

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Query Match          42.6%; Score 20; DB 6; Length 6;
Best Local Similarity 75.0%; Pred. No. 6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      6 MDVD 9
        ||:|
Db      1 MDID 4

```

Search completed: August 23, 2004, 11:05:16  
Job time : 59 secs



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OM protein - protein search, using SW model

Run on: August 23, 2004, 10:53:41 ; Search time 31 Seconds  
(without alignments)  
14.988 Million cell updates/sec

Title: US-09-914-088-1  
Perfect score: 47  
Sequence: 1 EDGQWMDVD 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

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Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/2/iaa/5B COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	28	59.6	7 4	US-09-842-164A-12 Sequence 12, Appl
2	23	48.9	8 1	US-08-346-455B-47 Sequence 47, Appl
3	23	48.9	8 3	US-08-977-221-47 Sequence 47, Appl
4	23	48.9	8 4	US-09-483-831B-47 Sequence 47, Appl
5	23	48.9	8 5	PCT-US95-06613-47 Sequence 47, Appl
6	22	46.8	5 1	US-08-447-010-26 Sequence 26, Appl
7	22	46.8	6 1	US-08-421-155-8 Sequence 8, Appl
8	22	46.8	6 2	US-08-232-539D-26 Sequence 26, Appl
9	22	46.8	6 2	US-09-001-157-8 Sequence 8, Appl
10	22	46.8	7 4	US-09-187-859-1617 Sequence 1617, Ap
11	22	46.8	7 4	US-09-839-542B-1617 Sequence 1617, Ap
12	22	46.8	8 1	US-08-421-155-6 Sequence 6, Appl
13	22	46.8	8 1	US-08-571-985-20 Sequence 20, Appl
14	22	46.8	8 1	US-08-487-860-60 Sequence 60, Appl
15	22	46.8	8 2	US-09-116-766-20 Sequence 20, Appl
16	22	46.8	8 2	US-09-001-157-6 Sequence 6, Appl
17	22	46.8	8 4	US-09-187-859-1623 Sequence 1623, Ap
18	22	46.8	8 4	US-09-839-542B-1623 Sequence 1626, Ap
19	22	46.8	9 4	US-09-187-859-1626 Sequence 1626, Ap
20	22	46.8	9 4	US-09-839-542B-1626 Sequence 5, Appl
21	21	44.7	7 4	US-09-308-453-5 Sequence 26, Appl
22	21	44.7	8 1	US-08-571-985-26 Sequence 26, Appl
23	21	44.7	8 2	US-09-116-766-26 Sequence 25, Appl
24	21	44.7	9 3	US-09-371-710-25 Sequence 25, Appl
25	21	44.7	9 3	US-09-648-386-25 Sequence 2, Appl
26	20	42.6	6 5	PCT-US93-00418-2 Sequence 36, Appl
27	20	42.6	8 2	US-08-286-819A-36

28	20	42.6	8 3	US-08-980-357-36 Sequence 36, Appl
29	20	42.6	8 4	US-09-460-384-13 Sequence 13, Appl
30	20	42.6	9 2	US-08-480-229C-17 Sequence 17, Appl
31	20	42.6	9 2	US-08-658-225C-17 Sequence 17, Appl
32	20	42.6	9 4	US-09-187-859-2405 Sequence 2405, Ap
33	20	42.6	9 4	US-09-839-542B-2405 Sequence 30, Appl
34	19	40.4	6 1	US-08-180-209B-30 Sequence 30, Appl
35	19	40.4	6 2	US-08-672-610A-35 Sequence 35, Appl
36	19	40.4	6 3	US-08-474-853-30 Sequence 30, Appl
37	19	40.4	6 4	US-09-166-205B-30 Sequence 30, Appl
38	19	40.4	6 4	US-09-608-790-6 Sequence 6, Appl
39	19	40.4	6 5	PCT-US94-02629-30 Sequence 30, Appl
40	19	40.4	7 1	US-07-968-781A-87 Sequence 87, Appl
41	19	40.4	7 2	US-08-672-610A-38 Sequence 38, Appl
42	19	40.4	7 3	US-08-293-728-18 Sequence 18, Appl
43	19	40.4	7 3	US-09-421-868-18 Sequence 18, Appl
44	19	40.4	7 4	US-09-535-852-1147 Sequence 1147, Ap
45	19	40.4	7 6	US-09-535-852-1147 Patent No. 5284931

## ALIGNMENTS

RESULT 1  
US-09-842-164A-12  
; Sequence 12, Application US/09842164A  
; Patent No. 6544754  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE, SATOSHI  
; TITLE OF INVENTION: LUTICERASE AND PHOTOPROTEIN  
; FILE REFERENCE: 206497050  
; CURRENT APPLICATION NUMBER: US/09/842,164A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: JP 2000-125053  
; PRIOR FILING DATE: 2000-04-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Ophiophorus graciliorostis  
; US-09-842-164A-12

Query Match 59.6%; Score 28; DB 4; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQWMDVD 9  
Db 1 GDWMDVD 7

RESULT 2  
US-08-346-455B-47  
; Sequence 47, Application US/08346455B  
; Patent No. 573167  
; GENERAL INFORMATION:  
; APPLICANT: UNITED STATES OF AMERICA; DEPT.  
; APPLICANT: OF HEALTH AND HUMAN SERVICES  
; TITLE OF INVENTION: MOTILITY STIMULATING  
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
DESCRIPTION: No
HYPOTHETICAL: No
FEATURE:
NAME/KEY: ATX-216
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-346-455B-47

Query Match      48.9%; Score 23; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 758-4800
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
DESCRIPTION: No
HYPOTHETICAL: No
FEATURE:
NAME/KEY: ATX-216
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-47

Query Match      48.9%; Score 23; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      3 GQVMD 7
      ||:|
Db      3 GQLMD 7

RESULT 3
US-08-977-221-47
; Sequence 47, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
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US-09-483-831B-47
; Sequence 47, Application US/09483831B
; Patent No. 6417338
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY
; APPLICANT: LIOTTA, LANCE
; APPLICANT: SCHIFFMANN, ELLIOTT
; APPLICANT: KRUTZCH, HENRY
; APPLICANT: MURATA, JUN
; TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
; TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2026-4149US4
; CURRENT APPLICATION NUMBER: US/09/483,831B
; CURRENT FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: 07/822,043
; PRIOR FILING DATE: 1992-01-17
; PRIOR APPLICATION NUMBER: 08/249,182
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/346,455
; PRIOR FILING DATE: 1994-11-28
; PRIOR APPLICATION NUMBER: 08/977,221
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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OTHER INFORMATION: Peptide  
US-09-483-831B-47

Query Match 48.9%; Score 23; DB 4; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQVMD 7  
||:|  
Db 3 GQLMD 7

RESULT 5  
PCT-US95-06613-47  
; Sequence 47, Application PC/TUS9506613  
; GENERAL INFORMATION:  
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;  
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,  
; APPLICANT: HENRY; MURATA, JUN  
; TITLE OF INVENTION: MOTILITY STIMULATING  
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/06613  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,455  
; FILING DATE: 28-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,182  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/822,043  
; FILING DATE: 17-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOROTHY R. ROTH  
; REGISTRATION NUMBER: 36,434  
; REFERENCE/DOCKET NUMBER: 2026-4149US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acids  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; DESCRIPTION: Peptide  
; HYPOTHEICAL: NO  
; FEATURE:  
; NAME/KEY: ATX-216  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PCT-US95-06613-47  
Query Match 48.9%; Score 23; DB 5; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GQVMD 7  
||:|  
Db 3 GQLMD 7

RESULT 6  
US-08-447-010-26  
; Sequence 26, Application US/08447010  
; Patent No. 5770718  
; GENERAL INFORMATION:  
; APPLICANT: MOFFATT, BARBARA  
; TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 330 University Avenue, Suite 701  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,010  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/230,695  
; FILING DATE: 21-APR-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/888,132  
; FILING DATE: 26-MAY-1992  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEWART, MICHAEL I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1811-183 MIS.vg  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; TELEX: 065-24567 SIMBAS  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-447-010-26  
Query Match 46.8%; Score 22; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQ 4  
|||  
Db 1 EDGQ 4  
RESULT 7  
US-08-421-155-8  
; Sequence 8, Application US/08421155  
; Patent No. 5703057  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Michael A.  
; APPLICANT: Lai, Wayne C.  
; APPLICANT: Johnston, Stephen A.

TITLE OF INVENTION: Expression Library Immunization  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/421,155  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kitchell, Barbara S.  
 REGISTRATION NUMBER: 33,928  
 REFERENCE/DOCKET NUMBER: UTSD:411/KIT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (713) 789-2679  
 TELEX: 79-0924  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-421-155-8

Query Match 46.8%; Score 22; DB 1; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 0;

QY 3 GQVMD 7  
 |||  
 Db 2 GQILD 6

RESULT 8  
 US-08-232-539D-26  
 Sequence 26, Application US/08232539D  
 Patent No. 5965709  
 GENERAL INFORMATION:  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Jardiou, Paula M.  
 TITLE OF INVENTION: 19E Antagonists  
 NUMBER OF SEQUENCES: 60  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/232,539D  
 FILING DATE: 21-Apr-1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/178583  
 FILING DATE: 07-JAN-1994  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: F0718P3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: linear  
 US-08-232-539D-26

Query Match 46.8%; Score 22; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

QY 1 EDGQ 4  
 |||  
 Db 3 EDGQ 6

RESULT 9  
 US-09-001-157-8  
 Sequence 8, Application US/09001157  
 Patent No. 5989553  
 GENERAL INFORMATION:  
 APPLICANT: Johnston, Stephen A.  
 APPLICANT: Barry, Michael A.  
 APPLICANT: Lal, Wayne C.  
 TITLE OF INVENTION: EXPRESSION LIBRARY IMMUNIZATION  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/001,157  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/421,155  
 FILING DATE: 07-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kitchell, Barbara S.  
 REGISTRATION NUMBER: 33,928  
 REFERENCE/DOCKET NUMBER: UTXD:529  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 512/418-3000  
 TELEFAX: 512/474-7577  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-09-001-157-8

Query Match 46.8%; Score 22; DB 2; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 0;

QY 3 QGVMD 7  
|:|  
Db 2 GQILD 6

## RESULT 10

US-09-187-859-1617  
; Sequence 1617, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1617  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
US-09-187-859-1617

Query Match 46.8%; Score 22; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QGVMD 9  
|:|  
Db 2 QINDVD 7

## RESULT 11

US-09-839-542B-1617  
; Sequence 1617, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Mathew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839,542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1617  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence  
US-09-839-542B-1617

Query Match 46.8%; Score 22; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QGVMD 9  
|:|  
Db 2 QINDVD 7

RESULT 12  
US-08-421-155-6  
; Sequence 6, Application US/08421155

; Patent No. 5703057  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Michael A.  
; APPLICANT: Lai, Wayne C.  
; APPLICANT: Johnston, Stephen A.  
; TITLE OF INVENTION: Expression Library Immunization  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/421,155  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UTSD:411/KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-421-155-6

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QGVMD 7  
|:|  
Db 2 GQILD 6

## RESULT 13

US-08-571-985-20  
; Sequence 20, Application US/08571985  
; Patent No. 5783557  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Yigal  
; APPLICANT: Trautman, Nathan  
; APPLICANT: Rycus, Avigail  
; TITLE OF INVENTION: THR-gamma2 Analogs and Pharmaceutical  
; TITLE OF INVENTION: Compositions Comprising Them  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Kohn & Associates  
; STREET: 30500 No. 5783557thwestern Hwy., Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48334  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/571,985  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 2163.00048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 539-5055  
TELEFAX: (810) 539-5055  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-571-985-20

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
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Db 2 EDGQ 5

RESULT 14  
US-08-487-860-60  
Sequence 60, Application US/08487860  
Patent No. 5792456  
GENERAL INFORMATION:  
APPLICANT: Yellon, Dale  
APPLICANT: Glaser, Scott  
APPLICANT: Huse, William  
APPLICANT: Rosok, Mae J.  
TITLE OF INVENTION: No. 5792456e1 Mutant BR96 Antibodies and  
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Merchant & Gould  
STREET: 11150 Santa Monica Blvd., Suite 400  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90025-3395  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,860  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436.16US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-487-860-60

Query Match 46.8%; Score 22; DB 1; Length 8;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMD 7  
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Db 2 QDGDITD 8

RESULT 15  
US-09-116-766-20  
Sequence 20, Application US/09116766  
Patent No. 5968898  
GENERAL INFORMATION:  
APPLICANT: Burstein, Yigal  
APPLICANT: Trainin, Nathan  
APPLICANT: Rykus, Avigail  
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
TITLE OF INVENTION: Compositions Comprising Them  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Kohn & Associates  
STREET: 30500 No. 5968898thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/116,766  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 2163.00050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-116-766-20

Query Match 46.8%; Score 22; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQ 4  
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Db 2 EDGQ 5

Search completed: August 23, 2004, 11:04:14  
Job time : 33 secs